

## RESULT 4

US-10-311-034-7  
; Sequence 7, Application US/10311034  
; Publication No. US20040023242A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YUE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BOROWSKY, Mark L.  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: LU, Yan  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: LU, Dyung Aina M.  
; APPLICANT: GREENWALD, Sara R.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: KEARNEY, Liam  
; APPLICANT: BUEFORD, Neil  
; APPLICANT: NGUYEN, Dannel B.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: HE, Ann  
; APPLICANT: THORNTON, Michael  
; APPLICANT: HAFALIA, April  
; APPLICANT: ARVIZU, Chandra S.  
; APPLICANT: GURURAJAN, Rajagopal  
; APPLICANT: LO, Terence P.  
; APPLICANT: KHAH, Farrah A.  
; APPLICANT: RECIPON, Shirley A.  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: POLICKY, Jennifer L.  
; APPLICANT: DING, Li  
; APPLICANT: GREYER, Megan  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: BATRA, Sajeev  
; APPLICANT: ISON, Craig H.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0125 PCT  
; CURRENT APPLICATION NUMBER: US/10/311,034  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
60/228,056  
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-15  
25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PERL Program  
; SEQ ID NO 7  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CD1  
US-10-311-034-7

Query Match 99.5%; Score 2589; DB 15; Length 497;  
Best Local Similarity 99.6%; Pred. No. 4.9e-189;  
Matches 495; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLKFYKARNPLDAGAAEPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60  
Db 1 MLKFYKARNPLDAGAAEPIASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60  
Qy 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHGFAEVQVVRKATG 120  
Db 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHGFAEVQVVRKATG 120

Qy 121 DIYAMKMKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKKHLYLVMEYQPG 180  
Db 121 DIYAMKMKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKKHLYLVMEYQPG 180  
Qy 181 DILSLANRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240  
Db 181 DILSLANRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240  
Qy 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGCLDCDMMWSVGVIAYEMIYGR 300  
Db 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGCLDCDMMWSVGVIAYEMIYGR 300  
Qy 301 SPFAEGTSARTFNNINFORFLKFPDDPKVSSFDLIIQSLLCGQKRLKPEGLCCHPPF 360  
Db 301 SPFAEGTSARTFNNINFORFLKFPDDPKVSSFDLIIQSLLCGQKRLKPEGLCCHPPF 360  
Qy 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPEKNVSWSSPCQLSPSGSGEELPFVGF 420  
Db 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPEKNVSWSSPCQLSPSGSGEELPFVGF 420  
Qy 421 YSKALGILGRSESVSGLDSPAKTSMWEKKLLIKSKELQDSQDKCHKVFTISAAGLLPCSR 480  
Db 421 YSKALGILGRSESVSGLDSPAKTSMWEKKLLIKSKELQDSQDKCHKVFTISAAGLLPCSR 480  
Qy 481 ILPSVYAKGSARGCWL 497  
Db 481 ILPSVYAKGSARGCWL 497

## RESULT 5

US-10-262-511-4  
; Sequence 4, Application US/10262511  
; Publication No. US20040038223A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John A.  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Ju, Jingfang  
; APPLICANT: Li, Li  
; APPLICANT: Guo, Xiaojia (Sasha)  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Ort, Tatiana  
; APPLICANT: Gorman, Linda  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Catterton, Elina  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Stone, David J.  
; APPLICANT: Pena, Carol E. A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Rothenberg, Mark E.  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Agee, Michele L.  
; APPLICANT: Berghs, Constance  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-462C  
; CURRENT APPLICATION NUMBER: US/10/262,511  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: 60/326,483  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: 60/373,815  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/327,917  
; PRIOR FILING DATE: 2001-10-09

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; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-511-4

Query Match          93.8%; Score 2440; DB 15; Length 623;
Best Local Similarity 99.6%; Pred. No. 1.5e-177;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60
Db 5 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 64
Qy 61 ECSQPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
Db 65 ECSQPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 124
Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Db 125 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 184
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTGHILKLVDF 240
Db 185 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTGHILKLVDF 244
Qy 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGCLDCDWMWSGVIAIYEMIYGR 300
Db 245 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGCLDCDWMWSGVIAIYEMIYGR 304
Qy 301 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFLDLIQSLICGKERLKFEGLCCHPFF 360
Db 305 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFLDLIQSLICGKERLKFEGLCCHPFF 364
Qy 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420
Db 365 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 424
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
Db 425 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 472

RESULT 6
US-10-028-946-4
; Sequence 4, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-05-17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-028-946-2

Query Match          93.8%; Score 2440; DB 13; Length 2054;
Best Local Similarity 99.8%; Pred. No. 6.7e-177;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60
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; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-028-946-4

Query Match          93.8%; Score 2440; DB 13; Length 1958;
Best Local Similarity 99.6%; Pred. No. 6.3e-177;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60
Db 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60
Qy 61 ECSQPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Db 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYOPGG 180
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTGHILKLVDF 240
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTGHILKLVDF 240
Qy 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGCLDCDWMWSGVIAIYEMIYGR 300
Db 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGCLDCDWMWSGVIAIYEMIYGR 300
Qy 301 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFLDLIQSLICGKERLKFEGLCCHPFF 360
Db 301 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFLDLIQSLICGKERLKFEGLCCHPFF 360
Qy 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420
Db 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468

RESULT 7
US-10-028-946-2
; Sequence 2, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-028-946-2

Query Match          93.8%; Score 2440; DB 13; Length 2054;
Best Local Similarity 99.8%; Pred. No. 6.7e-177;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60
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Db 1 MLKFKYGARNPLDAGAEPIASASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60  
Qy 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
Db 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
Qy 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180  
Db 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180  
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVVHRDIKPENILVDRTGHIKLVD 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVVHRDIKPENILVDRTGHIKLVD 240  
Qy 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWMWSVGVIAIYMIYGR 300  
Db 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWMWSVGVIAIYMIYGR 300  
Qy 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQSLLCGQKERLKFEGLCCHPFF 360  
Db 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQSLLCGQKERLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWVSSPCQLSPGSGEBELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWVSSPCQLSPGSGEBELPFVGF 420  
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 8

US-10-415-011-21  
; Sequence 21, Application US/10415011  
; Publication No. US20040053394A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE CORPORATION  
; APPLICANT: GURURAJAN, Rajagopal  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: XU, Yuming  
; APPLICANT: ARVIZU, Chandra S.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: DING, Li  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: HAFALIA, April J.A.  
; APPLICANT: NGUYEN, Dannel B.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: LU, Yan  
; APPLICANT: YUE, Henry  
; APPLICANT: BURFORD, Neil  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: Lal, Preeti G.  
; APPLICANT: RECIPON, Shirley A.  
; APPLICANT: Lu, Dyung Aina M.  
; APPLICANT: BOROWSKY, Mark L.  
; APPLICANT: THORNTON, Michael B.  
; APPLICANT: SWARNAKER, Anita  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: KHAN, Farrah A.  
; APPLICANT: ISON, Craig H.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0262 USN  
; CURRENT APPLICATION NUMBER: US/10/415,011  
; CURRENT FILING DATE: 2003-04-18  
; PRIOR FILING DATE: 2001-10-20  
; PRIOR APPLICATION NUMBER: PCT/US01/47728  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/242,410  
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: US 60/244,068  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/245,708  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/247,672  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US 60/249,565  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: US 60/252,730  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: US 60/250,807  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PERL Program  
; SEQ ID NO 21  
; LENGTH: 2054  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CD1  
US-10-415-011-21

Query Match 93.8%; Score 2440; DB 15; Length 2054;  
Best Local Similarity 99.6%; Pred. No. 6.7e-177;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLKFKYGARNPLDAGAEPIASASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60  
Db 1 MLKFKYGARNPLDAGAEPIASASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60  
Qy 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
Db 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
Qy 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180  
Db 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180  
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVVHRDIKPENILVDRTGHIKLVD 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVVHRDIKPENILVDRTGHIKLVD 240  
Qy 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWMWSVGVIAIYMIYGR 300  
Db 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWMWSVGVIAIYMIYGR 300  
Qy 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQSLLCGQKERLKFEGLCCHPFF 360  
Db 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQSLLCGQKERLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWVSSPCQLSPGSGEBELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWVSSPCQLSPGSGEBELPFVGF 420  
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 9

US-10-017-216-2  
; Sequence 2, Application US/10017216  
; Publication No. US20020160483A1  
; GENERAL INFORMATION:  
; APPLICANT: KAPPELLER-LIBERMANN, Rosana  
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot  
; FILE REFERENCE: 10147-57U1  
; CURRENT APPLICATION NUMBER: US/10/017,216  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/242,429  
; PRIOR FILING DATE: 2000-10-23

; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2053  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-216-2

Query Match 93.4%; Score 2430; DB 13; Length 2053;

Best Local Similarity 99.1%; Pred. No. 3.9e-176;

Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60  
Db 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60  
Qy 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
Qy 121 DIYAMKMKKALLAQEQVFFFEERNILSRSTSPWIPOLQYAFQDKNHLVMEYQPGG 180  
Db 121 DIYAMKMKKALLAQEQVFFFEERNILSRSTSPWIPOLQYAFQDKNHLVMEYQPGG 180  
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240  
Qy 241 GSAAKNSNMVNAKLPIGTPTYMAPEVLTVMNGDGKGTGYGLDCDWMWSGVIAIYMIYGR 300  
Db 241 GSAAKNSNMVNAKLPIGTPTYMAPEVLTVMNGDGKGTGYGLDCDWMWSGVIAIYMIYGR 300  
Qy 301 SPFAEGTSARTFNINMFORFLKPPDDPKVSSDFLDLIQSLCCQKRLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNINMFORFLKPPDDPKVSSDFLDLIQSLCCQKRLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCOLSPSGFSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCOLSPSGFSGEELPFVGF 420  
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQDKCHKV 468  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQDKCHKM 468

## RESULT 10

US-10-325-430-12  
; Sequence 12, Application US/10325430  
; Publication No. US20030153525A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Rosenfeld, Julie Beth  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,  
; TITLE OF INVENTION: 32838, 336 and 52908  
; FILE REFERENCE: MPI01-294P1ENM  
; CURRENT APPLICATION NUMBER: US/10/325,430  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/341,953  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 2053  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-325-430-12

Query Match 93.4%; Score 2430; DB 14; Length 2053;  
Best Local Similarity 99.1%; Pred. No. 3.9e-176;  
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

## RESULT 11

US-10-757-262-52  
; Sequence 52, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karichetti, Venkateswarlu  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Eliasof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,  
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30305, 2045, 16405, 18560, 2047,  
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,  
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22454, 2387, 52908, 69112, 14990,  
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,  
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,  
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,  
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
; FILE REFERENCE: MPI03-007PIRNMNIM  
; CURRENT APPLICATION NUMBER: US/10/757,262  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/444,783  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/478,742  
; PRIOR FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/488,529  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/491,156  
; PRIOR FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 60/499,594  
; PRIOR FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US 60/506,332



; PRIOR FILING DATE: 2003-09-26	
; NUMBER OF SEQ ID NOS: 136	
; SOFTWARE: Fast-SEQ for Windows Version 4.0	
; SEQ ID NO 52	
; LENGTH: 2053	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
; US-10-757-262-52	
Query Match 93.4%; Score 2430; DB 16; Length 2053;	
Best Local Similarity 99.1%; Pred. No. 3.9e-176;	
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	
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DB	1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60
QY	61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
DB	61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
QY	121 DIYAMKMKKALLAQAQVSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180
DB	121 DIYAMKMKKALLAQAQVSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180
QY	181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTHGHIKLVD 240
DB	181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTHGHIKLVD 240
QY	241 GSAAKMNSNMVNAKLPIGTDPYMAPEVLTVNMGDKGTGYGLDCDWMVGVIAEMYIGR 300
DB	241 GSAAKMNSNMVNAKLPIGTDPYMAPEVLTVNMGDKGTGYGLDCDWMVGVIAEMYIGR 300
QY	301 SPFAEGTSARTFNINMFQFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
DB	301 SPFAEGTSARTFNINMFQFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
QY	361 SKIDWNINRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGBELPVGFS 420
DB	361 SKIDWNINRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGBELPVGFS 420
QY	421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
DB	421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
RESULT 12	
US-10-618-941-67	
; Sequence 67, Application US/10618941	
; Publication No. US20040197792A1	
; GENERAL INFORMATION:	
; APPLICANT: WHYTE, DAVID	
; APPLICANT: MANNING, GERARD	
; APPLICANT: CAENEPEEL, SEAN	
; TITLE OF INVENTION: NOVEL KINASES	
; FILE REFERENCE: 034536-0321	
; CURRENT APPLICATION NUMBER: US/10/618,941	
; PRIOR FILING DATE: 2003-07-15	
; PRIOR APPLICATION NUMBER: 60/395,632	
; NUMBER OF SEQ ID NOS: 143	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 67	
; LENGTH: 2055	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
; US-10-618-941-67	
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Best Local Similarity 98.9%; Pred. No. 2.9e-175;	
Matches 464; Conservative 3; Mismatches 1; Indels 1; Gaps 1;	
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DB	1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60
QY	61 ECSQPALMKIKHVSNFVRK-YSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKAT 119
DB	61 ECSQPALMKIKHVSNFVRK-YSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKAT 120
QY	120 GDIYAMKMKKALLAQAQVSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 179
DB	121 GDIYAMKMKKALLAQAQVSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180
QY	180 GDIYAMKMKKALLAQAQVSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 239
DB	181 GDIYAMKMKKALLAQAQVSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 240
QY	240 GSAAKMNSNMVNAKLPIGTDPYMAPEVLTVNMGDKGTGYGLDCDWMVGVIAEMYIG 299
DB	241 GSAAKMNSNMVNAKLPIGTDPYMAPEVLTVNMGDKGTGYGLDCDWMVGVIAEMYIG 300
QY	300 RSPFAEGTSARTFNINMFQFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 359
DB	301 RSPFAEGTSARTFNINMFQFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
QY	360 FSKIDWNINRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGBELPVG 419
DB	361 FSKIDWNINRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGBELPVG 420
QY	420 SYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
DB	421 SYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 469
RESULT 13	
US-09-964-956-11	
; Sequence 11, Application US/09964956	
; Publication No. US20040043926A1	
; GENERAL INFORMATION:	
; APPLICANT: Gerlach, Valerie L	
; APPLICANT: MacDougall, John R	
; APPLICANT: Smithson, Glenna	
; APPLICANT: Willet, Isabelle	
; APPLICANT: Stone, David	
; APPLICANT: Gunther, Erik	
; APPLICANT: Blierman, Karen	
; APPLICANT: Grosse, William M	
; APPLICANT: Alsbrook II, John P	
; APPLICANT: Lepley, Denise M	
; APPLICANT: Burgess, Catherine E	
; APPLICANT: Padigaru, Muralidhara	
; APPLICANT: Kekuda, Ramesh	
; APPLICANT: Spytek, Kimberly A	
; APPLICANT: Leach, Martin D	
; APPLICANT: Shimkets, Richard A	
; TITLE OF INVENTION: No. US20040043926A1	
; FILE REFERENCE: 21402-124	
; CURRENT APPLICATION NUMBER: US/09/964,956	
; PRIOR FILING DATE: 2001-09-26	
; PRIOR APPLICATION NUMBER: 60/235,631	
; PRIOR FILING DATE: 2000-09-27	
; PRIOR APPLICATION NUMBER: 60/235,633	
; PRIOR FILING DATE: 2000-09-27	
; PRIOR APPLICATION NUMBER: 60/235,808	
; PRIOR FILING DATE: 2000-09-27	
; PRIOR APPLICATION NUMBER: 60/236,064	
; PRIOR FILING DATE: 2000-09-27	
; PRIOR APPLICATION NUMBER: 60/236,065	
; PRIOR FILING DATE: 2000-09-27	
; PRIOR APPLICATION NUMBER: 60/236,066	
; PRIOR FILING DATE: 2000-09-27	
; PRIOR APPLICATION NUMBER: 60/236,135	
; PRIOR FILING DATE: 2000-09-28	
; PRIOR APPLICATION NUMBER: 60/237,434	
; PRIOR FILING DATE: 2000-10-03	

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; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,396
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/276,667
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294,823
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/304,868
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-956-11

Query Match          92.7%; Score 2412.5; DB 11; Length 2053;
Best Local Similarity 98.9%; Pred. No. 8.4e-175;
Matches 463; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60
Db 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60

Qy 61 ECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180
Db 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180

Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSLMGYVHRDIKPENILVDRGTGHKLVDF 240
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSLMGYVHRDIKPENILVDRGTGHKLVDF 240

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Db 241 GSAAKNKNMKNVNAKLPIGTPDYMAPEVLTVMGDGGKTYGLDCDWMWSGVIAIYEMTYGR 300

Qy 301 SPFAEGTSARTFNIMNFQRLKPPDPKYSDDFLDLIQSLCGQKRLKFEGLCCHPFF 360
Db 301 SPFAEGTSARTFNIMNFQRLKPPDPKYSDDFLDLIQSLCGQKRLKFEGLCCHPFF 360

Qy 361 SKIDWNIRNSPPFVPTLSDDDTSNFDPEKNWSVSSPCQLSPSGFSGEELPFVGF 420
Db 361 SKIDWNIRNSPPFVPTLSDDDTSNFDPEKNWSVSSPCQLSPSGFSGEELPFVGF 420

Qy 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468
Db 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKM 467
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## RESULT 14

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US-10-262-511-2
; Sequence 2, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Rameen
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
```

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; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-2

Query Match          92.7%; Score 2412.5; DB 15; Length 2053;
Best Local Similarity 98.9%; Pred. No. 8.4e-175;
Matches 463; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

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Db 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE 60

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Db 61 ECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180
Db 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180

Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSLMGYVHRDIKPENILVDRGTGHKLVDF 240
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSLMGYVHRDIKPENILVDRGTGHKLVDF 240

Qy 241 GSAAKNKNMKNVNAKLPIGTPDYMAPEVLTVMGDGGKTYGLDCDWMWSGVIAIYEMTYGR 300
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Qy 361 SKIDMNNIRNSPPFPVPTLKSDDTNSFDEPEKNSWSSSPCQLSPSGFSGEELPFVGF 420
Db 360 SKIDMNNIRNSPPFPVPTLKSDDTNSFDEPEKNSWSSSPCQLSPSGFSGEELPFVGF 419
Qy 421 YSKALGILGRSESVWSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
Db 420 YSKALGILGRSESVWSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 467

RESULT 15
US-09-964-956-9
; Sequence 9, Application US/09964956
; Publication No. US20040043926A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Szytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/09/964,956
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,396
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/276,667
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294,823
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/304,868
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2066
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-964-956-9
Query Match 92.7%; Score 2412.5; DB 11; Length 2066;
Best Local Similarity 98.9%; Pred. No. 8.5e-175;
Matches 463; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQKQPPFMTQQQMSPLSREGILDALFVLF 60
Db 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQKQPPFMTQQQMSPLSREGILDALFVLF 60
Qy 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKOFEVRSLVGCGHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKCSDTIAELQELQPSAKOFEVRSLVGCGHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKALLAQOVSFFFEERNILSRSTSPWIPQLQYAPQDKNHLVLMVEYOPGG 180
Db 121 DIYAMKVMKKALLAQEQVSFFFEERNILSRSTSPWIPQLQYAPQDKNHLVLMVEYOPGG 180
Qy 181 DLLSLNRYEDQLDENLIQFYLAELILAVHSLVHLMGYVHRDIKPENILVDRTHIKLVDF 240
Db 181 DLLSLNRYEDQLDENLIQFYLAELILAVHSLVHLMGYVHRDIKPENILVDRTHIKLVDF 240
Qy 241 GSAAKWNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGVLDCDMMWSVGVIAYEMIYGR 300
Db 241 GSAAKWNSNK-VNAKLPIGTPDYMAPEVLTVMNGDGKGTGVLDCDMMWSVGVIAYEMIYGR 299
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Db 300 SPFAEGTSARTFNNIMNFQFLKPPDDPKVSSDFDLDIQLLCCGQERLKFEGLCCHPPF 359
Qy 361 SKIDMNNIRNSPPFPVPTLKSDDTNSFDEPEKNSWSSSPCQLSPSGFSGEELPFVGF 420
Db 360 SKIDMNNIRNSPPFPVPTLKSDDTNSFDEPEKNSWSSSPCQLSPSGFSGEELPFVGF 419
Qy 421 YSKALGILGRSESVWSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
Db 420 YSKALGILGRSESVWSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 467

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Job time : 148 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 18, 2005, 15:31:31 ; Search time 44 Seconds  
(without alignments)  
843.195 Million cell updates/sec

Title: US-10-724-594-2

Perfect score: 2602

Sequence: 1 MLKFKYGARNPLDAGAAEPI.....CSRILPSVYAKSGARGCWL 497

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2602	100.0	497	4	US-10-238-709-2
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4	2440	93.8	2054	4	US-10-028-946-2
5	2271.5	87.3	494	4	US-09-804-471A-4
6	2271.5	87.3	494	4	US-10-238-709-4
7	1284	49.3	257	4	US-09-916-204-2
8	1284	49.3	257	4	US-10-282-048-2
9	1180	45.3	251	4	US-09-916-204-4
10	1180	45.3	251	4	US-10-282-048-4
11	1177	45.2	251	4	US-09-916-204-5
12	1177	45.2	251	4	US-09-916-204-6
13	1177	45.2	251	4	US-10-282-048-5
14	1177	45.2	251	4	US-10-282-048-6
15	894.5	34.4	509	4	US-09-949-016-8511
16	865	33.2	1388	2	US-08-685-576-4
17	865	33.2	1388	4	US-09-976-594-296
18	864.5	33.2	1354	3	US-08-685-871-2
19	860.5	33.1	1388	2	US-08-685-576-1
20	857.5	33.0	420	3	US-08-685-871-58
21	840.5	32.3	420	3	US-08-685-871-59
22	828	31.8	582	2	US-08-422-699A-9
23	828	31.8	582	2	US-08-422-706B-9
24	790.5	30.4	900	2	US-08-630-822A-62
25	790.5	30.4	900	2	US-09-005-069-62
26	790.5	30.4	900	3	US-09-171-156A-21
27	790.5	30.4	900	4	US-09-004-730A-21

28	790.5	30.4	900	4	US-08-981-799A-21	Sequence 21, Appl
29	771.5	29.7	638	2	US-08-422-699A-11	Sequence 11, Appl
30	771.5	29.7	638	2	US-08-422-706B-11	Sequence 11, Appl
31	760.5	29.2	555	1	US-08-484-044-6	Sequence 6, Appl
32	711	27.3	479	3	US-09-442-100-13	Sequence 13, Appl
33	711	27.3	479	3	US-08-939-106-13	Sequence 13, Appl
34	711	27.3	479	3	US-09-442-102-13	Sequence 13, Appl
35	701	26.9	526	3	US-09-442-100-12	Sequence 12, Appl
36	701	26.9	526	4	US-08-939-106-12	Sequence 12, Appl
37	701	26.9	526	4	US-09-442-102-12	Sequence 12, Appl
38	686	26.4	719	3	US-09-588-256-2	Sequence 2, Appl
39	683	26.2	404	2	US-08-860-150-3	Sequence 3, Appl
40	683	26.2	404	3	US-09-338-132-3	Sequence 3, Appl
41	677	26.0	464	3	US-08-878-989-4	Sequence 4, Appl
42	677	26.0	464	3	US-09-272-796-4	Sequence 4, Appl
43	674.5	25.9	465	2	US-08-878-989-18	Sequence 18, Appl
44	674.5	25.9	465	2	US-08-860-150-7	Sequence 7, Appl
45	674.5	25.9	465	3	US-09-338-132-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-804-471A-2

; Sequence 2, Application US/09804471A

; Patent No. 6479269

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: CL001164

; CURRENT APPLICATION NUMBER: US/09/804,471A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 497

; TYPE: PRT

; ORGANISM: Human

US-09-804-471A-2

Query Match	100.0%;	Score 2602;	DB 4;	Length 497;
Best Local Similarity	100.0%;	Pred. No. 1.5e-242;		
Matches	497;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MLKFKYGARNPLDAGAAEPIANRASRLNLF	FQCKPPFTQQQMSPLSREGILDALFVLFE	60
Db	1	MLKFKYGARNPLDAGAAEPIANRASRLNLF	FQCKPPFTQQQMSPLSREGILDALFVLFE	60
Qy	61	ECSPALMKIKHVSNFVRKYSDTIAELOLPSAKDPEVRS	LVGCGHFAEVQVVRKATG	120
Db	61	ECSPALMKIKHVSNFVRKYSDTIAELOLPSAKDPEVRS	LVGCGHFAEVQVVRKATG	120
Qy	121	DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWI	POLYAFQDKNHLVLYMEYOPGG	180
Db	121	DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWI	POLYAFQDKNHLVLYMEYOPGG	180
Qy	181	DLLSLNRYVEDQDENLIFOYLAELILAVSHVLMGVHR	DIKPENILVDRTGHIKLVD	240
Db	181	DLLSLNRYVEDQDENLIFOYLAELILAVSHVLMGVHR	DIKPENILVDRTGHIKLVD	240
Qy	241	GSAAKNNSKNVNAKLPIGTPDYMAPEVLTVMNGDKG	TVGLDCDMSVGVIAEYMYGR	300
Db	241	GSAAKNNSKNVNAKLPIGTPDYMAPEVLTVMNGDKG	TVGLDCDMSVGVIAEYMYGR	300
Qy	301	SPPAEGTSARTFNINMNFORFLKFPDDPKVSSDFDL	LIQSLLCCQKLERLFCCHPFF	360
Db	301	SPPAEGTSARTFNINMNFORFLKFPDDPKVSSDFDL	LIQSLLCCQKLERLFCCHPFF	360
Qy	361	SKIDMWNIRNSPPFPVPTLKSDDDTNFDPEKNWSV	SSPCQLSPGSGEELPFGFS	420
Db	361	SKIDMWNIRNSPPFPVPTLKSDDDTNFDPEKNWSV	SSPCQLSPGSGEELPFGFS	420

Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSSPQLSPSGFSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELOSDQKCHKVFI SAAGLLPCSR 480  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELOSDQKCHKVFI SAAGLLPCSR 480  
QY 481 ILPSVYAKSGARGCWL 497  
Db 481 ILPSVYAKSGARGCWL 497

RESULT 2  
US-10-238-709-2  
; Sequence 2, Application US/10238709  
; Patent No. 6680188  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; CURRENT FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-10-238-709-2

Query Match 100.0%; Score 2602; DB 4; Length 497;  
Best Local Similarity 100.0%; Pred. No. 1.5e-242; Mismatches 0; Indels 0; Gaps 0;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLPFGKPPFTMQOQMSPLSREGILDALFVLF 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLPFGKPPFTMQOQMSPLSREGILDALFVLF 60  
QY 61 ECSQPALMKIKHVSFNVRKYSDDTIAELOELQPSAKDFEVSRLVGCCHGFAEVQVVRKATG 120  
Db 61 ECSQPALMKIKHVSFNVRKYSDDTIAELOELQPSAKDFEVSRLVGCCHGFAEVQVVRKATG 120  
QY 121 DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNKHLVLMVYOPGG 180  
Db 121 DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNKHLVLMVYOPGG 180  
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHIKLVDF 240  
QY 241 GSAAKNSKNMKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMSVGVIAEMVYGR 300  
Db 241 GSAAKNSKNMKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMSVGVIAEMVYGR 300  
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLIQSLICGQKERLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLIQSLICGQKERLKFEGLCCHPFF 360  
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSSPQLSPSGFSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSSPQLSPSGFSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELOSDQKCHKVFI SAAGLLPCSR 480  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELOSDQKCHKVFI SAAGLLPCSR 480  
QY 481 ILPSVYAKSGARGCWL 497  
Db 481 ILPSVYAKSGARGCWL 497

RESULT 3

US-10-028-946-4  
; Sequence 4, Application US/10028946  
; Patent No. 6734009  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1958  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-028-946-4

Query Match 93.8%; Score 2440; DB 4; Length 1958;  
Best Local Similarity 99.6%; Pred. No. 5.3e-226;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLPFGKPPFTMQOQMSPLSREGILDALFVLF 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLPFGKPPFTMQOQMSPLSREGILDALFVLF 60  
QY 61 ECSQPALMKIKHVSFNVRKYSDDTIAELOELQPSAKDFEVSRLVGCCHGFAEVQVVRKATG 120  
Db 61 ECSQPALMKIKHVSFNVRKYSDDTIAELOELQPSAKDFEVSRLVGCCHGFAEVQVVRKATG 120  
QY 121 DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNKHLVLMVYOPGG 180  
Db 121 DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNKHLVLMVYOPGG 180  
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHIKLVDF 240  
QY 241 GSAAKNSKNMKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMSVGVIAEMVYGR 300  
Db 241 GSAAKNSKNMKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMSVGVIAEMVYGR 300  
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLIQSLICGQKERLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLIQSLICGQKERLKFEGLCCHPFF 360  
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSSPQLSPSGFSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSSPQLSPSGFSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELOSDQKCHKV 468  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELOSDQKCHKV 468

RESULT 4  
US-10-028-946-2  
; Sequence 2, Application US/10028946  
; Patent No. 6734009  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 4

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-2

Query Match      93.8%; Score 2440; DB 4; Length 2054;
Best Local Similarity 99.6%; Pred. No. 5.7e-226;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKQPPFMTQQQMSPLSREGILDALFVLFE 60
DB 1 MLKFKYGARNPLDAGAAEPTASRASRLNLFQKQPPFMTQQQMSPLSREGILDALFVLFE 60
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMYQPGG 180
DB 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMYQPGG 180
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTGHIKLVD 240
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTGHIKLVD 240
QY 241 GSAAKNNSNMVNAKLPIGTPDYMAPEVLTVMGDGGKTYGLDCDWMWSGVIAIYMIYGR 300
DB 241 GSAAKNNSNMVNAKLPIGTPDYMAPEVLTVMGDGGKTYGLDCDWMWSGVIAIYMIYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLDIQSLLCGQKXERLKFEGLCCHPFF 360
DB 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSSDFDLDIQSLLCGQKXERLKFEGLCCHPFF 360
QY 361 SKIDWNNIRNSPPFPVPTLKSDDDTSNFDEPEKNWSVSSPCQLSPGSGEELPFVGF 420
DB 361 SKIDWNNIRNSPPFPVPTLKSDDDTSNFDEPEKNWSVSSPCQLSPGSGEELPFVGF 420
QY 421 YSKALGILGRSSEVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKVFIISAGLLPCSR 480
DB 421 YSKALGILGRSSEVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKVFIISAGLLPCSR 480
QY 481 ILPSVYAKGSARGC 495
DB 480 ILQSIYAEGSAGHC 494

RESULT 6
US-10-238-709-4
; Sequence 4, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-238-709-4

Query Match      87.3%; Score 2271.5; DB 4; Length 494;
Best Local Similarity 87.3%; Pred. No. 1.2e-210;
Matches 432; Conservative 27; Mismatches 35; Indels 1; Gaps 1;

QY 1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQKQPPFMTQQQMSPLSREGILDALFVLFE 60
DB 1 MLKFKYGVNRNPPASASEPTASRASRLNLFQKQPPFMTQQQMSALSREGMLDALFALFE 60
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMYQPGG 180
DB 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMYQPGG 180
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTGHIKLVD 240
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTGHIKLVD 240
QY 241 GSAAKNNSNMVNAKLPIGTPDYMAPEVLTVMGDGGKTYGLDCDWMWSGVIAIYMIYGR 300
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Db 241 GSAAKMSNK-VDAKLPFGDYNAPVLTVMNDRGTGYLDCDWSVGVAEMVYK 299  
Qy 301 SPFAEGTSARTFNIMNFORLKPDPDPKVSDDFLDIQSLCCQKRLKFEGLCCHPFF 360  
Db 300 TPFTEGTSARTFNIMNFORLKPDPDPKVSSELDDLQSLLCVKERLKFEGLCCHPFF 359  
Qy 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420  
Db 360 ARTDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWAFILCVPAEPLAFSGEELPFVGF 419  
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFI-SAAGLLPCSR 480  
Db 420 YSKALGILGRSESVVSSLDSPAKVSMEKKLLIKSKELQSDQKCHKVISTAGLRPCSR 479  
Qy 481 ILPSVYAKGSARGC 495  
Db 480 ILQSIYAEGSAGHC 494

## RESULT 7

US-09-916-204-2  
; Sequence 2, Application US/09916204  
; Patent No. 6638745  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164CIP  
; CURRENT APPLICATION NUMBER: US/09/916,204  
; CURRENT FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Human  
US-09-916-204-2

Query Match 49.3%; Score 1284; DB 4; Length 257;  
Best Local Similarity 99.6%; Pred. No. 1.1e-115;  
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
Qy 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
Db 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
Qy 121 DIYAMKMKKALLAQEQVSFFFEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180  
Db 121 DIYAMKMKKALLAQEQVSFFFEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180  
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSLMGVYVHRDIKPENILVDRTGHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSLMGVYVHRDIKPENILVDRTGHIKLVDF 240  
Qy 241 GSAAKMNSNMV 252  
Db 241 GSAAKMNSNMV 252

## RESULT 8

US-10-282-048-2  
; Sequence 2, Application US/10282048  
; Patent No. 6692948  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001164CIP-DIV  
; CURRENT APPLICATION NUMBER: US/10/282,048  
; CURRENT FILING DATE: 2002-10-29  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Human  
US-10-282-048-2

Query Match 49.3%; Score 1284; DB 4; Length 257;  
Best Local Similarity 99.6%; Pred. No. 1.1e-115;  
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
Qy 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
Db 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
Qy 121 DIYAMKMKKALLAQEQVSFFFEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180  
Db 121 DIYAMKMKKALLAQEQVSFFFEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180  
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSLMGVYVHRDIKPENILVDRTGHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSLMGVYVHRDIKPENILVDRTGHIKLVDF 240  
Qy 241 GSAAKMNSNMV 252  
Db 241 GSAAKMNSNMV 252

## RESULT 9

US-09-916-204-4  
; Sequence 4, Application US/09916204  
; Patent No. 6638745  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164CIP  
; CURRENT APPLICATION NUMBER: US/09/916,204  
; CURRENT FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-916-204-4

Query Match 45.3%; Score 1180; DB 4; Length 251;  
Best Local Similarity 90.4%; Pred. No. 1.2e-105;  
Matches 227; Conservative 13; Mismatches 11; Indels 0; Gaps 0;  
Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
Qy 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
Db 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
Qy 121 DIYAMKMKKALLAQEQVSFFFEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180  
Db 121 DIYAMKMKKALLAQEQVSFFFEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180





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; Sequence 5, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-282-048-5

Query Match      45.2%; Score 1177; DB 4; Length 251;
Best Local Similarity 90.0%; Pred. No. 2.4e-105;
Matches 226; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MLKFYGARPLDAGAAEPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60
Db 1 MLKFYGVRRPPEASASEPIASRASRLNLFQGGKPLMTQQQMSALSREGMLDALFALFE 60

Qy 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSARDFEVRSVLCGCHFAEVQVVRKATG 120
Db 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSARDFEVRSVLCGCHFAEVQVVRKATG 120

Qy 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLYLVMEYQPGG 180
Db 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLYLVMEYQPGG 180

Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240
Db 181 DFLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240

Qy 241 GSAAKMNSNM 251
Db 241 GSAAKMNSNKV 251

; ORGANISM: Mus musculus
; US-10-282-048-6

Query Match      45.2%; Score 1177; DB 4; Length 251;
Best Local Similarity 90.0%; Pred. No. 2.4e-105;
Matches 226; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MLKFYGARPLDAGAAEPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60
Db 1 MLKFYGVRRPPEASASEPIASRASRLNLFQGGKPLMTQQQMSALSREGMLDALFALFE 60

Qy 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSARDFEVRSVLCGCHFAEVQVVRKATG 120
Db 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSARDFEVRSVLCGCHFAEVQVVRKATG 120

Qy 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLYLVMEYQPGG 180
Db 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLYLVMEYQPGG 180

Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240
Db 181 DFLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240

Qy 241 GSAAKMNSNM 251
Db 241 GSAAKMNSNKV 251

; ORGANISM: Mus musculus
; US-10-282-048-6

Query Match      45.2%; Score 1177; DB 4; Length 251;
Best Local Similarity 90.0%; Pred. No. 2.4e-105;
Matches 226; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MLKFYGARPLDAGAAEPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLF 60
Db 1 MLKFYGVRRPPEASASEPIASRASRLNLFQGGKPLMTQQQMSALSREGMLDALFALFE 60

Qy 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSARDFEVRSVLCGCHFAEVQVVRKATG 120
Db 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSARDFEVRSVLCGCHFAEVQVVRKATG 120
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Db 61 ECSOPALMKIKHVSFVRKYSDTIAELQELQPSARDFEVRSVLCGCHFAEVQVVRKATG 120
Qy 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLYLVMEYQPGG 180
Db 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLYLVMEYQPGG 180
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240
Db 181 DFLSLNRYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTHGHIKLVDF 240
Qy 241 GSAAKMNSNM 251
Db 241 GSAAKMNSNKV 251

RESULT 15
US-09-949-016-8511
; Sequence 8511, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8511
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8511

Query Match      34.4%; Score 894.5; DB 4; Length 509;
Best Local Similarity 38.8%; Pred. No. 1.4e-77;
Matches 187; Conservative 93; Mismatches 145; Indels 57; Gaps 9;

Qy 31 FQCKP-----PFMTQQQMSPLSREGILDALFVFECCQPAL 67
Db 1 FQCKPAEIANMSGEVRLQEQFILDGPAQTNGQC--FSVETLLDILICLYDECNNSP 58

Qy 68 MKIKHVSFVRKYSDTIAELQELQPSARDFEVRSVLCGCHFAEVQVVRKATGDIYAMKV 127
Db 59 REKNILEVLEWAKPFTSKVQKMLHREDFEILKVLGRGAFGEVAVVKLNADKVFAMKI 118

Qy 128 MKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLYLVMEYQPGGDLISLN 187
Db 119 LNKWMLKRAETACPREERDVLVNGDNKWTTLHYAFQDNNLYLVMDYVVGDLTLLS 178

Qy 188 RYEDQDENLIQFYLAELILAVHSHVLMGYVHRDIKPENILVDRTHGHIKLVDFGSAKMN 247
Db 179 KPEDRLPEDMARFYLAEMVIAIDSVHQLHYVHRDIKPDNLMDMNGHILRADFGSLCKLM 238

Qy 248 SNKMVNAKLPIGTPDYMAPEVLTVMGDKGTGYGLDQDMSVGVIAIYEMLYGRSPFAEGT 307
Db 239 EDGTVOSSVAVGTPDIYSPEILOAME-DKGRYGPCDMSVGVIAIYEMLYGRSPFAEGT 297

Qy 308 SARTFNNIMNFORFLKPPDD-PKVSSDFLDLIQSLCGQKRLKFEGL---CCHPFSKI 363
Db 298 LVETGYKIMNHERFQFPAQVTDVSENKDLIRRLICSRHRLGNGIEDFKKHPPFSGI 357

Qy 364 DNNINRNSPPFPVTLKSDDDTSNDEPE---KNSWSSSPCOLSPSGSGBELPVGFS 420
Db 358 DMDNIRNCBAPYIPEVSSPTDTSNFDVDDDDCLKNSETMPPPP---THTAFSGHHLPVGFT 414

Qy 421 YSKALGILGRS-----ESVSVGLDSPAKTSSMEKKL-----LIKSKELQ 459
```

Db 415 YTS:CVLSDRSCLRVTAGPTSLDLDVNVQFTLDNNLATEAVERRIKLEQEKLELSKLO 474  
QY 460 DS 461  
Db 475 ES 476

Search completed: March 18, 2005, 15:41:38  
Job time : 45 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:22:34 ; Search time 174 Seconds  
(without alignments)  
1462.663 Million cell updates/sec

Title: US-10-724-594-2

Perfect score: 2602

Sequence: 1 MLKFKYGARNPLDAGAAEPI.....CSRILPSVYAKGARGRCWL 497

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2440	93.8	2027	2 Q86UQ9	Q86UQ9 homo sapien
2	2425	93.2	482	2 Q6XUJ8	Q6XUJ8 homo sapien
3	2271.5	87.3	494	2 Q88937	Q88937 mus musculus
4	2172.5	83.5	2055	2 Q88938	Q88938 mus musculus
5	2157.5	82.9	448	2 Q88527	Q88527 rattus norv
6	929	35.7	717	2 Q8AVM0	Q8AVM0 xenopus lae
7	929	35.7	1551	2 Q6DT37	Q6DT37 homo sapien
8	922	35.4	1854	2 Q9VTV8	Q9VTV8 drosophila
9	897.5	34.5	1592	2 Q01583	Q01583 caenorhabdi
10	896.5	34.5	492	2 Q86XZ8	Q86XZ8 homo sapien
11	896.5	34.5	933	2 Q86TJ1	Q86TJ1 homo sapien
12	896.5	34.5	1711	2 Q9YSS2	Q9YSS2 homo sapien
13	896.5	34.5	1760	2 Q9ULU5	Q9ULU5 homo sapien
14	891	34.2	496	2 Q99646	Q99646 homo sapien
15	891	34.2	1573	2 Q7PV87	Q7PV87 anopheles g
16	891	34.2	1638	2 Q86XX2	Q86XX2 homo sapien
17	891	34.2	1719	2 Q86XX3	Q86XX3 homo sapien
18	891	34.2	1732	2 Q54874	Q54874 rattus norv
19	890	34.2	1638	2 Q81WQ7	Q81WQ7 homo sapien
20	883	33.9	1702	2 Q54875	Q54875 rattus norv
21	883	33.9	1713	2 Q7TWT49	Q7TWT49 rattus norv
22	880	33.8	1713	2 Q7TWT50	Q7TWT50 mus musculus
23	876.5	33.7	1173	2 P92199	P92199 caenorhabdi
24	874	33.6	1370	2 Q73732	Q73732 xenopus lae
25	867	33.3	1375	2 Q90Y37	Q90Y37 brachydanio
26	866.5	33.3	1354	1 ROC1_MOUSE	ROC1_MOUSE mus musculus
27	865	33.2	1388	1 ROC2_HUMAN	ROC2_HUMAN homo sapien
28	864.5	33.2	1354	1 ROC1_HUMAN	ROC1_HUMAN homo sapien
29	862.5	33.1	1369	1 ROC1_RAT	ROC1_RAT rattus norv
30	860.5	33.1	1354	1 ROC1_RABIT	ROC1_RABIT o rbo-assoc
31	860.5	33.1	1388	1 ROC2_BOVIN	ROC2_BOVIN bos taurus

RESULT 1

ID	Q86UQ9	PRELIMINARY;	PRT;	2027 AA.
AC	Q86UQ9;			
DT	01-JUN-2003 (Tremblrel. 24, Created)			
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Rho/rac-interacting citron kinase.			
GN	Names=CIT;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Huang C.Q., Wu S.L., Shan Y.X., Liu S., Xiao P.J.;			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
CC	-!- SIMILARITY: Contains 1 PH domain.			
DR	EMBL; AY257469; AAP13528.1; -			
DR	HSSP; P31751; 1MRV			
DR	GO; GO:0005622; C:intracellular; IEA.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0005083; F:small GTPase regulatory/interacting protein. . ; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR	GO; GO:0004668; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR001180; Citron.			
DR	InterPro; IPR005479; C:phosphorylation; IEA.			
DR	InterPro; IPR002219; DAG PE-bind.			
DR	InterPro; IPR011009; Kinase_like.			
DR	InterPro; IPR001849; PH.			
DR	InterPro; IPR000961; Kinase_C.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR000861; REM repeat.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	InterPro; IPR008271; Ser_thr_pkin_AS.			
DR	Pfam; PF00130; CL_1; 1.			
DR	Pfam; PF00780; CNH; 1.			
DR	Pfam; PF00169; PH; 1.			
DR	Pfam; PF00069; Kinase; 1.			
DR	Pfam; PF00433; Kinase_C; 1.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00109; CL_1; 1.			
DR	SMART; SM00036; CNH; 1.			
DR	SMART; SM00233; PH; 1.			
DR	SMART; SM00220; S_TKc; 1.			
DR	SMART; SM00133; S_TKc; 1.			
DR	PROSITE; PS00867; GTPase_2; UNKNOWN 1.			
DR	PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.			
DR	PROSITE; PS0081; DAG_PE_BIND_DOM_2; 1.			
DR	PROSITE; PS0003; PH_DOMAIN; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			

ALIGNMENTS

Q6P526 homo sapien  
Q44368 drosophila  
Q9W1B0 mus musculus  
P70336 mus musculus  
P54265 mus musculus  
Q62868 rattus norv  
Q90013 homo sapien  
Q961D4 drosophila  
Q9U779 drosophila  
Q9VXE3 drosophila  
Q98A66 gallus gall  
Q00565 homo sapien  
Q6D171 mus musculus  
Q6L535 oryza sativ

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DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 2027 AA; 231429 MW; 6B1D8C3F661F357B CRC64;

Query Match 93.8%; Score 2440; DB 2; Length 2027;
Best Local Similarity 99.6%; Pred. No. 5.7e-153; Indels 0; Gaps 0;
Matches 466; Conservative 2; Mismatches 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180
Db 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180
QY 181 DLSLLNRYEDQDENLIQFYLAELILAVHSLVHLMGYVHRDIKPNILVDRTGHIKLVDF 240
Db 181 DLSLLNRYEDQDENLIQFYLAELILAVHSLVHLMGYVHRDIKPNILVDRTGHIKLVDF 240
QY 241 GSAAKNSNKNVNAKPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDWSVGVIAIYMIYGR 300
Db 241 GSAAKNSNKNVNAKPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDWSVGVIAIYMIYGR 300
QY 301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFDLIQSLLCGQKERLKFEGLCCHPFF 360
Db 301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFDLIQSLLCGQKERLKFEGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGBELPFVGF 420
Db 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGBELPFVGF 420
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
Db 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 2
Q6XUH8
ID Q6XUH8 PRELIMINARY; PRT; 482 AA.
AC Q6XUH8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Citron Rho-interacting kinase short form.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Mao Y., Xie Y., Wu Q.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AV209000; AAP43922.1; -.
DR HSSP; P05132; IATP.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002230; Ser Thr kinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.

DR PROSITE; PS00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 482 AA; 54353 MW; 4F02AF6A32C73BAE CRC64;

Query Match 93.2%; Score 2425; DB 2; Length 482;
Best Local Similarity 98.9%; Pred. No. 9.2e-153; Indels 0; Gaps 0;
Matches 463; Conservative 3; Mismatches 2;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180
Db 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180
QY 181 DLSLLNRYEDQDENLIQFYLAELILAVHSLVHLMGYVHRDIKPNILVDRTGHIKLVDF 240
Db 181 DLSLLNRYEDQDENLIQFYLAELILAVHSLVHLMGYVHRDIKPNILVDRTGHIKLVDF 240
QY 241 GSAAKNSNKNVNAKPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDWSVGVIAIYMIYGR 300
Db 241 GSAAKNSNKNVNAKPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDWSVGVIAIYMIYGR 300
QY 301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFDLIQSLLCGQKERLKFEGLCCHPFF 360
Db 301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFDLIQSLLCGQKERLKFEGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGBELPFVGF 420
Db 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGBELPFVGF 420
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468
Db 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 3
O88937
ID O88937 PRELIMINARY; PRT; 494 AA.
AC O88937;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rho/rac-interacting citron kinase short isoform.
GN NamesCit; Synonyms=Crik-sk;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99009084; PubMed=972683; DOI=10.1074/jbc.273.45.29706;
RA Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,
RA Dotto G.P.;
RT "Citron rho-interacting kinase, a novel tissue-specific ser/thr kinase
RL J. Biol. Chem. 273:29706-29711(1998).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF086823; AAC72822.1; -.
DR HSSP; P31751; 1MRV.
DR MGD; MGI:105313; Cit.
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DR GO: 0005524; F:ATP binding; IEA.
DR GO: 0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: 0016740; F:transferase activity; IEA.
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR00961; Kinase_C.
DR InterPro: IPR00719; Prot_kinase.
DR InterPro: IPR02290; Ser_thr_pkinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR Pfam: PF00069; Pkinase; I.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00133; S_TK_X; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 494 AA; 55742 MW; 2C60D2294B28A185 CRC64;

Query Match      87.3%; Score 2271.5; DB 2; Length 494;
Best Local Similarity 87.3%; Pred. No. 1.5e-142;
Matches 432; Conservative 27; Mismatches 35; Indels 1; Gaps 1;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFMTQQQMSPLSREGILDALFVLF 60
DB 1 MLKFKYGVNRNPPASASEPIASRASRLNLFQCKPPLMTQQQMSALSREGMLDALFAL 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYOPGG 180
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYOPGG 180
QY 181 DLSLLNRYEDQDLENLIQFYLAELILAVHSLVHLMGVVHRDIKPENILVDRTHIKLVDF 240
DB 181 DLSLLNRYEDQDLENLIQFYLAELILAVHSLVHLMGVVHRDIKPENILVDRTHIKLVDF 240
QY 241 GSAAKNNSKQVNAKLPDTPDMABEVLTVMGDGGTYGLDCDWMVSGVIAEYMIYGR 300
DB 241 GSAAKNNSKQVNAKLPDTPDMABEVLTVMGDGGTYGLDCDWMVSGVIAEYMIYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKPPDDPKVSSDFDLIQLSLCGOKERLKFGLCCHPFF 360
DB 300 TPTEGTSARTFNINMFORFLKPPDDPKVSSDFDLIQLSLCGOKERLKFGLCCHPFF 359
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTNSFDEPEKNSWSSSPCQLSPSGFSGBELPFVGF 420
DB 360 ARTDWNIRNSPPFPVPTLKSDDDTNSFDEPEKNSWAFILCVPAEPLAFSGBELPFVGF 419
QY 421 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFTISAAGLPCSR 480
DB 420 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFTISAAGLPCSR 479
QY 481 ILPSVYAKSGARGRC 495
DB 480 ILSIYAEGSAGGHC 494

RESULT 4
RE8938 PRELIMINARY; PRT; 2055 AA.
ID O88938
AC O88938;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Rho/rac-interacting citron kinase.
GN Name=Cit; Synonyms=Crik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=99009084; PubMed=9792683; DOI=10.1074/jbc.273.45.29706;
RA Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,
RA Dotto G.P.;
RT "Citron rho-interacting kinase, a novel tissue-specific ser/thr kinase
RT encompassing the Rho-Rac-binding protein Citron."
RL J. Biol. Chem. 273:29706-29711(1998).
CC 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC 1- SIMILARITY: Contains 1 PH domain.
DR ENMBL: AF086824; AAC72823.1; -.
DR HSSP: P31751; 1MRV.
DR MGD: MGI:105313; Cit.
DR GO: 0005622; C:intracellular; IEA.
DR GO: 0005524; F:ATP binding; IEA.
DR GO: 0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: 0005083; F:small GTPase regulatory interacting protein. .; IEA.
DR GO: 0016740; F:transferase activity; IEA.
DR GO: 0007242; P:intracellular signaling cascade; IEA.
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR001180; Citron.
DR InterPro: IPR005479; Cphp_synth_L_D2.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR000861; REM_repeat.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00130; Cl_1; 1.
DR Pfam: PF00780; CNH; 1.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR00194; TROPOMYOSIN.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00109; Cl; 1.
DR SMART: SM00036; CNH; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00133; S_TK_X; 1.
DR PROSITE: PS00867; CPKASE_2; UNKNOWN_1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00003; PH_DOMAIN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 2055 AA; 235480 MW; 2120CB5E454DA940 CRC64;

Query Match      83.5%; Score 2172.5; DB 2; Length 2055;
Best Local Similarity 88.0%; Pred. No. 3.3e-135;
Matches 412; Conservative 26; Mismatches 29; Indels 1; Gaps 1;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFMTQQQMSPLSREGILDALFVLF 60
DB 1 MLKFKYGVNRNPPASASEPIASRASRLNLFQCKPPLMTQQQMSALSREGMLDALFAL 60
QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYOPGG 180
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYOPGG 180
QY 181 DLSLLNRYEDQDLENLIQFYLAELILAVHSLVHLMGVVHRDIKPENILVDRTHIKLVDF 240
DB 181 DLSLLNRYEDQDLENLIQFYLAELILAVHSLVHLMGVVHRDIKPENILVDRTHIKLVDF 240

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Db 181 DFLSLNRYEDQDDESMIQFYLAELILAVHSHVQMGVYVHRDIKIPENILIDRTGEIKLVDF 240
QY 241 GSAKKNNSKNNVNAKPIGTPTDYMADPEVLTVMGDGKGTGYGLDCDWWSGVGVIAEYMYGR 300
Db 241 GSAKKNNSK-VDAKUPIGTPTDYMADPEVLTVMGDEDRGTGYGLDCDWWSGVGVIAEYMYGK 299
QY 301 SPAEGTSARTFNNINMFORFLKFPDDPKVSSDFDLIQLLCCGQKRLKFEGLCCHPFF 360
Db 300 TPTEGTSARTFNNINMFORFLKFPDDPKVSSDLDDLQLLCCGQKRLKFEGLCCHPFF 359
QY 361 SKIDMNNIRNSPPFPVTLKSDDDTNSFDEPEKNSWSSPCQLSPGSGFSGEELPFVGF 420
Db 360 ARTDNNIRNSPPFPVTLKSDDDTNSFDEPEKNSWAFILCVPAEPLAFSGEELPFVGF 419
QY 421 YSKALGILGRSESVSGSLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468
Db 420 YSKALGILGRSESVSGSLDSPAKTSSMEKLLIKSKELQDSQDKCHKM 467

RESULT 5
Q88527 PRELIMINARY; PRT; 448 AA.
AC Q88527;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Citron-K kinase (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Madaule P., Eda M., Watanabe N., Fujisawa K., Matsuoka T., Bito H.,
RA Ishizaki T., Narumiya S.;
RT "Role of Citron kinase as a target of the small GTPase Rho in
RL cytolysis."
RL Nature 0:0-0(1998).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR ENBL; AF070065; AAC27932.1; -.
DR HSSP; P31751; IMRV.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000961; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; I.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 448 448
SQ SEQUENCE 448 AA; 50650 MW; 548CA5AEAE4A6394 CRC64;

Query Match 82.98; Score 2157.5; DB 2; Length 448;
Best Local Similarity 90.98; Pred. No. 4.8e-135;
Matches 408; Conservative 21; Mismatches 19; Indels 1; Gaps 1;

QY 1 MLKFKYGARNPLDAGAEPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLF 60
Db 1 MLKFKYGVNPSASAEPIASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLF 60
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKQPEVRSVLCGGHFARVQVREKATG 120
Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKQPEVRSVLCGGHFARVQVREKATG 120

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## RESULT 6

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Q8AVM0 PRELIMINARY; PRT; 717 AA.
AC Q8AVM0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cdc42bpb protein (Fragment).
GN Name=Cdc42bpb;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative."
RL Dev. Dyn. 225:384-391(2002).

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RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC041741; AAH41741.1; -.
DR HSP; P49137; INXK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00059; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM0133; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 717
SQ SEQUENCE 717 AA; 83371 MW; 2D295D4A8A5B733A CRC64;

Query Match 35.7%; Score 929; DB 2; Length 717;
Best Local Similarity 41.7%; Pred. No. 3.1e-53;
Matches 196; Conservative 84; Mismatches 148; Indels 42; Gaps 10;

QY 23 RASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLEECSPALMKIKHVSFV---RK 79
DB 6 RLKRLLEQLLDGP-----QRNEAVSVETLIDVLCLYCTESTSLTRDKYVSFLEWAKP 61

QY 80 YSDTIAELQBLQPSAKDFVRSVLCGHFAEVOVVRKATGDIYAMVKMKKALLAQEQV 139
DB 62 FTDL---LKGQMLHRDDFEIIKVIGRGAFAVAVRLKSTERIYAMKILNKWEMLKRAET 118

QY 140 SFPEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGDLSLLNRYEDQDENLIQ 199
DB 119 ACFREERNVLVNGDCQWITTLHYAFQDENLYLVMDYVVGDLTLTLKPEDRLPEDMSR 178

QY 200 FYLAELILAVSHVLMGYVHRDIKPENILVDRTGHIKLVDFGSAAMKSNKMNNAKLPIC 259
DB 179 FYLAEMVLATHSIQLHYVHRDIKPDNILLDMNGHIRLADFGSLKMKNGDGTVOSSVAVG 238

QY 260 TPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMIVGRSPFAETGTSARTFNINMFQ 319
DB 239 TPDYISPEILLQAME-DGMGKYGPECDSWGLVCMYEMLYGETFPYAESLVETGKIMNHE 297

QY 320 RFLKFPDD-PKVSDFDLQLSLCGQKRLKFEGL---CCHPFFSKIDWNINRNSPPPF 375
DB 298 ERQFPFHIGDVSESADKLQRLICSRERRLQNGIDDFKAHPFFEGIDWNIRNLEAPY 357

QY 376 VPTLKSDDDTSNDEPE---KNWSVSSPCQLSPGSGEELFVGFYSYK-----423
DB 358 IPDVSPSPDTSNFDVDDILLRNEVTPSS---THSGFSGFHLFPFVGFTYTTDCSFDGRGS 414

QY 424 -----ALGILGRESVSVGLSDSPAKTSMBKKL-----LIKSKELQDS 461'
DB 415 LKDTIHANATVKDEDVQRGLQNSLOVDYERRIRRELEQKLELNRLKQES 464

RESULT 7
Q6DT37
ID Q6DT37 PRELIMINARY; PRT; 1551 AA.
AC Q6DT37
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Myotonic dystrophy kinase-related CDC42-binding kinase gamma.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ng Y., Tan I., Lim L., Leung T.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; AY648038; AAT67172.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG PE-bind.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKbox/RhoBind.
DR InterPro; IPR011849; PH-related.
DR InterPro; IPR011036; PH-related.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00659; Pkinase; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; SM00036; CNH; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00479; DAG PE BIND DOM_1; UNKNOWN_1.
DR PROSITE; PS50081; DAG PE BIND DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1551 AA; 172517 MW; 6B2DCED7BF57B1E CRC64;

Query Match 35.7%; Score 929; DB 2; Length 1551;
Best Local Similarity 43.8%; Pred. No. 8.2e-53;
Matches 184; Conservative 83; Mismatches 125; Indels 28; Gaps 7;

QY 49 EGLDIALFVLEECSPALMKIKHVSFVVKYKSDTIAELQELQPSAKDFVRSVLCGHF 108
DB 23 DGLDILLALHHEHSSGLRRRSVAQFVSKVKELRLQDRDDFEILKVIKRGAF 82

QY 109 AEYQVVRKATGDIYAMVKMKKALLAQEQVSPFEEERNILSRSTSPWIPOLQYAFQDKN 168
DB 83 GEVTVVRQDTGQIFAMKMLHKWEMLKRAETACFREERDVLVKGDNRWVTLHYAQDBE 142

QY 169 HLYLVMEYQPGDLSLLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENIL 228
DB 143 YLYLVMDYVYAGDILLTLRFRDLPPPELAQFYLAEMVLAIHSLHQLGYVHRDVKPDNL 202

QY 229 VDETGHILKLVDRGSAAMKSNKMNNAKLPITGPDYMAPEVLTVNMGDKGTGYGLDCDWS 288
DB 203 LDVNGHIRLADFGSLRLNTNGMVDSSVAVGTPDYISPEILQAME-EGKGHYGPQCDDWS 261

QY 289 VGVYAYEMIVGRSPFAETGTSARTFNINMFQRLKFPDD-PKVSSDFDLILQSLCCQKE 347

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QY 110 EVQVREKATGDIYAMKVMKKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKH 169
DB 126 NVHLVVERQNDIYAMKKIKKSVVTSQ----VKEERDIMSINSEWNLINLQYAFQDNND 181
QY 170 LYLVMVEQPGDILLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILV 229
DB 182 LYLVMVEQPGDILLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILV 240
QY 230 DRGTHIKLVDFGSAAKNSNKNVNAKLPICTPDYMAPEVLTVMNGD--GKGTGYGLDCDMW 287
DB 241 DRGTHIKLVDFGSAAKNSNKNVNAKLPICTPDYMAPEVLTVMNGD--GKGTGYGLDCDMW 300
QY 288 SVGIYAYEMIGYSPFAEGTSARTFNNIM-----NFQRELFKPPDPKPVSSDFLDLIQSL 341
DB 301 SMGIIGVELICETTPHEDNVHETYSKILSCHESHLKELISFPADLKVSNNYRNIESL 360
QY 342 LCQOKERLKEGLCCCHPFFSKIDWNIRNSPPFPVPTLSDDDTSNPFDE-----PEKN 394
DB 361 VTNPCKLSYERIKNHPFFSEIPWGSIRSQVPPPIPTVRSDDDTSNFEDGIRHKTREQG 420
QY 395 SWYSSPCOLSPSGFSGEELPPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIK 454
DB 421 VAKSLITNMKSNDFSGKLPFGISFVH-----WEKSAISATTDKLEQK 466
QY 455 SKEL 458
DB 467 LKEL 470

RESULT 9
O01583
ID O01583 PRELIMINARY; PRT; 1592 AA.
AC O01583;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Temporally assigned gene name protein 59.
GN Name:tag-59; ORFNames=K08B12.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG Wormbase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Becker M., Wohldmann P.;
RT "The sequence of C. elegans cosmid K08B12.5";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RT Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG Wormbase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

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CC -!- SIMILARITY: Contains 1 PH domain.
DR EMBL; U97001; AAB52260.3; -.
DR PIR; T25808; T25808.
DR HSSP; P49137; INXK.
DR WormBase; WEGene00006437; K08B12.5.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKbox/RhoBndng.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
- KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1592 AA; 180743 MW; F909FA8F5C9C876C CRC64;

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Query Match 34.5%; Score 897.5; DB 2; Length 1592;
Best Local Similarity 40.5%; Pred. NO. 1e-50;
Matches 178; Conservative 91; Mismatches 150; Indels 21; Gaps 8;

QY 28 NLFFQGGKPPFTQQQMSPLSRREGILDALFVLFECSQPALMKIKHYSNFVKYSDTIAEL 87
DB 19 NIYMDG-----PSKKPEALSFFETLIDSLICLYDECCNSTLRKEKTAEPVESVKTWISKA 73
QY 88 QELQPSAKDFEVRSLVGCGHFAEVQVVRKATGDIYAMKVMKKKALLAQEQVSPFEERN 147
DB 74 KKLRLSRDDDFEVLKVIKGAFGEVAVVRMGVGEIYAMKLNKWNKVAETACFREED 133
QY 148 ILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGDILLNRYEDQDENLQFYLAELIL 207
DB 134 VLVYGDRRWITNLHVAFOQDEKNLYFVMDYIIGDMLTLLSKFVDHHPESMAKFIYAEWVL 193
QY 208 AVHSVHLMGYVHRDIKPNILVDRGTHIKLVDFGSAAKNSNKNVNAKLPICTPDYMAPE 267
DB 194 AIDSLHRLGYVHRDVKPDNVLDMQGHIRLADFGSCLRLADGSAVSNVAVGPPDYISPE 253
QY 268 VLTVMNGDGKGTGYGLDCDMWSVGVTAYEMIGYSPFAEGTSARTFNNIMNFORFLKPPDD 327
DB 254 ILRAME-DGRGYGKEDMWSLIGI CNYEMLYGTTTPYSERLVDTYTKIKSHQDMLDFPDD 312
QY 328 P---KVSSDFLDLIQSLCGQKERLKEGLC---CHPFFSKIDWNIRNSPPFPVPTLKS 381
DB 313 EIDWVYVEEAKOLIRQLICSSDVRFGNGLSDFQLHPPFPEGIDWNTIRDSNPPYVPEVSS 372
QY 382 DDDTSNPFDEPEKNWSVSSPC--QLSP-----SGFSGEELPFVGFSYSKALGILGRSESV 435
DB 373 PEDTSNFDVDCED--DFTPCLOEQTPRVLAFTGNHLFPVGFYSYTHG--SLLSARSLSLT 429

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Qy 436 SGLDSPARTSMKMLIKS 455
Db 430 DEIRAIAQCGDAELMEKS 449

RESULT 10
Q86XZ8 PRELIMINARY; PRT; 492 AA.
AC
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CDC42BPB protein (Fragment).
GN Name=CDC42BPB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR ENBL; BC048261; AAH48261.1; -
DR HSSP; P31751; IMRY.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser Thr_kinase.
DR Pfam; PF00089; Kinase; 1.
DR Pfam; PF00433; Kinase C; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S TK; 1.
DR SMART; SM00133; S TK X; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 492
SQ SEQUENCE 492 AA; 5F9FD9CC1D2AEFC CRC64;

Query Match 34.5%; Score 896.5; DB 2; Length 492;
Best Local Similarity 42.1%; Pred. No. 2.8e-51;
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RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strauberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC047871; AB47871.1; -.
DR HSSP; P31751; IMRY.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000961; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; I.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 933
SQ SEQUENCE 933 AA; 108543 MW; 38E7179C3253F521 CRC64;

Query Match 34.5%; Score 896.5; DB 2; Length 933;
Best Local Similarity 42.1%; Pred. No. 6.2e-51;
Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;

QY 44 SPLSREGILDALVLFEECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLV 103
DB 23 SALSVELLDVLVCLTECHSALRDKYVAEFLWAKPFTQLVKEMQLHREDFEIKVI 82

QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYA 163
DB 83 GRGAFGEVAVVKMNTERIYAMKILNKWEMLKRAETACPREERDVLVNGDCQWITALHYA 142

QY 164 FQDKHLYLWMEYQPGGDLISLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIK 223
DB 143 FQDENHLYLWMDYYVGGDLTLTSKPEDKLPEDMARFYIGEMVLAIDSIHQHLYVHRDIK 202

QY 224 PENILVDRTHIKLVDFGSAAKNSKMNKVNNAKLPIDGTPYMAPEVLTVMNGDGKGYGLD 283
DB 203 PDNVLLDVNGHRLADFGSLCKNDGTQVSSVAVGTPDYISPEILQAME-DGNGKYGPE 261

QY 284 CDWWSVGVIAYEMIGRSPAEGTSAFTNINMFORFLKFPDD-PKVSSDFDLQSL 342
DB 262 CDWWSLGVCMYEMLYGETPYAESLVETYGKIMNHEERFQPSHVTDVSEAKDLIQRLL 321

QY 343 CGQKERLKEGL---CCHPEFSKIDNNINRSPFPVPTLKSDDDTNSDEPE---KNSW 396
DB 322 CSRRERLQNGIEDFKKAFHFEGLAWENIRNLEAPYIPDVSSPSDTSNFDVDDVLNTE 381

QY 397 VSSSPQLSP---SGFSGBELPWFVGSYKALGILGRSEWSGLDSPAKTSSMEKKLLI 453
DB 382 I-----LPGSHGTFSGHLHPFGFTFT-----TSCFS--DRGSLKSIQSNVTLT 425

QY 454 KSKELQSDQKCHKVFISA 472
DB 426 KQEDVQ--RDLEHSLQWEA 442

RESULT 12
QY552 PRELIMINARY; PRT; 1711 AA.
AC QY552;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CDC42-binding protein kinase beta.

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GN Name=CDC42BPB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99216425; PubMed=10198171; DOI=10.1006/geno.1999.5769;
RA Moncrieff C.L., Bailey M.E., Morrison N., Johnson K.J.;
RT "Cloning and chromosomal localization of human Cdc42-binding protein kinase beta.";
RL Genomics 57:297-300(1999).
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF128625; AAD37506.1; -.
DR HSSP; P31751; IMRY.
DR GO; GO:0005856; C:cytoskeleton; TAS.
DR GO; GO:0004672; F:protein kinase activity; TAS.
DR GO; GO:0007163; P:establishment and/or maintenance of cell po. .; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_P8-bind.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000095; PAKbox/RhoBindng.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00008; DAGEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1711 AA; 194356 MW; 3A3731D40A363497 CRC64;

Query Match 34.5%; Score 896.5; DB 2; Length 1711;
Best Local Similarity 42.1%; Pred. No. 1.3e-50;
Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;

QY 44 SPLSREGILDALVLFEECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLV 103
DB 23 SALSVELLDVLVCLTECHSALRDKYVAEFLWAKPFTQLVKEMQLHREDFEIKVI 82

QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYA 163
DB 83 GRGAFGEVAVVKMNTERIYAMKILNKWEMLKRAETACPREERDVLVNGDCQWITALHYA 142

QY 164 FQDKHLYLWMEYQPGGDLISLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIK 223
DB 143 FQDENHLYLWMDYYVGGDLTLTSKPEDKLPEDMARFYIGEMVLAIDSIHQHLYVHRDIK 202

QY 224 PENILVDRTHIKLVDFGSAAKNSKMNKVNNAKLPIDGTPYMAPEVLTVMNGDGKGYGLD 283
DB 203 PDNVLLDVNGHRLADFGSLCKNDGTQVSSVAVGTPDYISPEILQAME-DGNGKYGPE 261

QY 284 CDWWSVGVIAYEMIGRSPAEGTSAFTNINMFORFLKFPDD-PKVSSDFDLQSL 342
DB 262 CDWWSLGVCMYEMLYGETPYAESLVETYGKIMNHEERFQPSHVTDVSEAKDLIQRLL 321

QY 343 CGQKERLKEGL---CCHPEFSKIDNNINRSPFPVPTLKSDDDTNSDEPE---KNSW 396
DB 322 CSRRERLQNGIEDFKKAFHFEGLAWENIRNLEAPYIPDVSSPSDTSNFDVDDVLNTE 381

QY 397 VSSSPQLSP---SGFSGBELPWFVGSYKALGILGRSEWSGLDSPAKTSSMEKKLLI 453
DB 382 I-----LPGSHGTFSGHLHPFGFTFT-----TSCFS--DRGSLKSIQSNVTLT 425

QY 454 KSKELQSDQKCHKVFISA 472
DB 426 KQEDVQ--RDLEHSLQWEA 442

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Db 262 CDWLSGLVCWYEMLYGETFFVAESLVETYGKIMNHHERFQPPSHVTDVSEAKDLIQRLLI 321
Qy 343 CGQKERLKFEGL-----CCHPPFSKIDMNNIRNSPPFPVFTLKSDDDTSNFDPEPE---KNSW 396
Db 322 CSRRRLRGNGIEDFKKHAFFEGLNWENIRLEAPYIPDVSSPSDTSNFDVDDVLRNTE 381
Qy 397 VSSSPCOLSP---SGFSGEELPFVGFYSYKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
Db 382 I-----LPPGSHYGFGLHLFPFGFTFT-----TESCFS--DRGSLKSIQSNLT 425
Qy 454 KSKELQSDQKCHKVFISA 472
Db 426 KDDEVQ--RDLEHSLQMEA 442

RESULT 13
Q9ULU5 PRELIMINARY; PRT; 1760 AA.
AC Q9ULU5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
GN KIAA1124 protein (Fragment).
DE Name=KIAA1124;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Brain;
RC MEDLINE=20039618; PubMed=10574461;
RA Hrosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis
RL from size-fractionated cDNA libraries from human brain.";
DNA Res. 6:329-336(1999).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; AB032950; BAA86438.2; -.
DR HSP; P31751; IMRY.
DR Gene; HGNC:1738; CDC42BPB.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR01180; Citron.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000095; PAKbox/Rho-binding.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00433; Kinase C; 1.
DR PRINTS; PR00008; DAGPEOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; Cl_1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
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DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1 1
SQ SEQUENCE 1760 AA; 199208 MW; 3A1CA9A7A4BF5FA3 CRC64;

Query Match 34.5%; Score 896.5; DB 2; Length 1760;
Best Local Similarity 42.1%; Pred. No. 1.4e-50;
Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;

Qy 44 SPLSREGILDALFVLPFCSCPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLV 103
Db 72 SALSVETLLDLVLCVTEGSHSALRRDKYVAFLEWAKPFTQLVKEMQLHREDFEIKVI 131
Qy 104 GCGHFAEVQVREKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYA 163
Db 132 GRGAFGEVAVVMKNTERTIYAMKILNKWELKRAETACFREERDVLVNGDCQWITALHYA 191
Qy 164 FQDKNHLVLMYEQGGDLLSLNRYEDQDENLQFYLAELIYAVHSLMGYVHRDIK 223
Db 192 FQDENHLVLMVDYVVGDLTLTLKFKEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 251
Qy 224 PENILVDRTHIKLVDPFGSAANKSNKMYNAKLPTGPDYMAPEVLTVMNGDGKGYGLD 283
Db 252 PDNLVLDVNGHIRLADFGSLKNDGTVQSSVAVGTPTYISPEILQAME-DGMGKYGPE 310
Qy 284 CDWWSVGVIAYEMIVGRSPFASTGTSARTENNIMNFORFLKFPDD-PKVSSDFDLIQSL 342
Db 311 CDWWSLVCWYEMLYGETFFVAESLVETYGKIMNHHERFQPPSHVTDVSEAKDLIQRLLI 370
Qy 343 CGQKERLKFEGL---CCHPPFSKIDMNNIRNSPPFPVFTLKSDDDTSNFDPEPE---KNSW 396
Db 371 CSRRRLRGNGIEDFKKHAFFEGLNWENIRLEAPYIPDVSSPSDTSNFDVDDVLRNTE 430
Qy 397 VSSSPCOLSP---SGFSGEELPFVGFYSYKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
Db 431 I-----LPPGSHYGFGLHLFPFGFTFT-----TESCFS--DRGSLKSIQSNLT 474
Qy 454 KSKELQSDQKCHKVFISA 472
Db 475 KDDEVQ--RDLEHSLQMEA 491

RESULT 14
Q99646 PRELIMINARY; PRT; 496 AA.
AC Q99646;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE Ser-thr protein kinase PK428.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao Y., Kidd V., Kraft A.S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDAJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; U59305; AAB37126.1; -.
DR HSP; P31751; IMRY.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
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DR Pfam; PF00433; Kinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 496 AA; 56991 MW; 069186D74AB9C936 CRC64;

Query Match 34.2%; Score 891; DB 2; Length 496;
Best Local Similarity 40.3%; Pred. No. 6.5e-51;
Matches 183; Conservative 92; Mismatches 145; Indels 34; Gaps 8;

QY 36 PFMTQOQMSPLSREGILDALFVFECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAK 95
DB 18 PAQTNGQY--FSVETLLDILICLYDCNNSPLREKNILEYLEWAKPFTSKVKQMLHRE 75
QY 96 DFEVRLVGCGHFAEVQVREKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSP 155
DB 76 DFEILKVICRGAFGEVAVVKLNADKVFAKILNKWMLKRAETACFREERDVLVNGDNK 135
QY 156 WIPQLOVAFQKXHLVMEYQGGDLILLNRYEDQDENLIQFYLAELILAVHSHLM 215
DB 136 WITTHYAFQDDNNLLVMDYVGGDLTLLSKFEDLPEDMARFYLAEMVIAIDSVHQL 195
QY 216 GYVHRDIPENILVDRTGHLKLVDFGSAAKWNNKMNNAKLPIGTDPYMAPEVLTVMNGD 275
DB 196 HYVHRDIKPNILMDNWHIRLADFGSLKMDGTQSSVAVGTDPYISPELQAME-D 254
QY 276 GKTYGLDCDWSGVYAYEMIGRSPFAEGTSARTFNINMFORFLKPPDD--PKYSSDF 334
DB 255 GKRGYGPCDWSLGVCMYEMLYGETPFYAESLVETVYGYKIMNHKRFQPPAQVTDVSENA 314
QY 335 LDLIQSLCCQKRELKPEGL---CCHPFFSKIDWNIRNSPPFPVTLKSDDDTSNDEP 391
DB 315 KOLIRLCSREHRLQONGIEDFKGHPFFSGIDWDNIRNCEAPYIPEVSSPTDTSNFDVD 374
QY 392 E---KNSVSSSSPQLSPSFGSGEELPFVFGFSYKALGILGRS-----ESV 434
DB 375 DDCCLKNSWTMPPP---THTAFSGHLLPFVFGFTTSSCVLSDRCLRVAGTSLDLDMNV 431
QY 435 VSGLSDPKTSMEKKL-----LIKSKELQDS 461
DB 432 QRTLDNNLATEAYERRIKLEQKELSRKLQES 465

RESULT 15
Q7PV87
ID Q7PV87 PRELIMINARY; PRT; 1573 AA.
AC Q7PV87;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE ENSANGP0000009214 (Fragment).
GN Name=ENSANGG00000006898;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008986; EAA00280.2; -.
DR HSSP; P31751; 1MRV.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
```

Search completed: March 18, 2005, 15:40:01  
Job time : 179 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:30:56 ; Search time 42 Seconds  
(without alignments)  
1138.565 Million cell updates/sec

Title: US-10-724-594-2  
Perfect score: 2602  
Sequence: 1 MLKFKYARNPLDAGAEPI.....CSRILPSVYAKSGARGCWL 497  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	908.5	34.9	1548	2 T25808	hypothetical prote
2	891	34.2	1732	2 T14039	protein kinase (EC
3	883	33.9	1702	2 T14050	protein kinase (EC
4	876.5	33.7	1173	2 T25539	hypothetical prote
5	866.5	33.3	1354	2 S74244	serine/threonine-s
6	864.5	33.2	1354	2 S69211	serine/threonine-s
7	863	33.2	624	2 B49364	protein kinase (EC
8	860.5	33.1	1388	2 S70533	serine/threonine-s
9	853.5	32.8	1388	2 S74245	serine/threonine-s
10	847	32.6	557	2 S71829	serine/threonine-s
11	721	27.7	522	2 G86431	protein kinase T51
12	711	27.3	479	2 S42864	protein kinase (EC
13	704	27.1	756	2 S60966	probable protein k
14	701	26.9	526	2 S49077	protein kinase PKT
15	700	26.9	469	2 T41723	serine/threonine-s
16	697	26.8	596	2 P84589	probable protein k
17	693	26.6	569	2 A86170	hypothetical prote
18	687.5	26.4	474	2 I78396	myotonic dystrophy
19	685	26.3	441	2 I78393	myotonic dystrophy
20	685	26.3	516	2 I78394	myotonic dystrophy
21	682.5	26.2	1356	2 T16718	hypothetical prote
22	676.5	26.0	443	2 D71405	probable protein k
23	676.5	26.0	475	2 H85156	protein kinase [im
24	674.5	25.9	465	2 I38133	protein kinase (EC
25	665.5	25.6	500	2 S42867	protein kinase (EC
26	660.5	25.4	483	2 T05188	protein kinase F4I
27	639	24.6	545	2 T01288	protein kinase F27
28	636.5	24.5	598	2 T47254	serine/threonine k
29	636.5	24.5	665	2 S70706	probable protein k

30	636	24.4	480	2 T47255	serine/threonine k
31	636	24.4	620	2 S22711	probable protein k
32	608	23.4	908	2 T25035	hypothetical prote
33	606.5	23.3	412	2 I78395	myotonic dystrophy
34	604	23.2	1099	2 A58155	tumor suppressor p
35	548	21.1	607	2 S62556	probable serine/th
36	536	20.6	624	2 T41341	probable serine/th
37	532.5	20.5	564	2 S59776	protein kinase DBF
38	522	20.1	572	2 S64387	protein kinase DBF
39	520.5	20.0	726	2 S22258	probable protein k
40	520	20.0	1092	2 H95509	protein F2/P5.23 l
41	516	19.8	893	2 S63378	hypothetical prote
42	515	19.8	425	2 S41099	protein kinase (EC
43	510.5	19.6	646	2 T38171	probable serine/th
44	510	19.6	462	1 T17287	protein kinase (EC
45	509	19.6	569	2 T50414	probable prolifera

ALIGNMENTS

RESULT 1

T25808  
hypothetical protein K08B12.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 16-Aug-2004  
C;Accession: T25808  
R;Becker, M.; Wohldmann, P.  
submitted to the EMBL Data Library, April 1997  
A;Description: The sequence of C. elegans cosmid K08B12.  
A;Reference number: Z20091  
A;Accession: T25808  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1548 <BEC>  
A;Cross-references: UNIPROT:O01583; EMBL:U97001; PIDN:AAB52260.1; GSPDB:GN00023; CESP:K08B12  
A;Experimental source: strain Bristol N2; clone K08B12  
C;Genetics:  
A;Gene: CESP:K08B12.5  
A;Map position: 5  
A;Introns: 39/1; 66/1; 156/3; 278/2; 391/3; 628/1; 1022/2; 1273/3; 1326/1; 1423/2; 1489/2;  
C;Superfamily: protein kinase homology  
F;956-1005/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match	34.9%;	Score	908.5;	DB 2;	Length	1548;
Best Local Similarity	40.6%;	Pred. No.	2.3e-33;			
Matches	178;	Conservative	91;	Mismatches	150;	Indels 19; Gaps 7;
QY	28	NLFQGGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAEL	87			
DB	19	NIYMDG-----PSKKEALSFETLIDSLICLYDECCNSTLRKEKIAEFVESVKTWISKA	73			
QY	88	QELQPSAKDFEVRSLVGCCHFAEVQVVRKATGDIYAMKVMKKALLAQEQVFFBEERN	147			
DB	74	KKLRSLRDDFEVLKVIKGAFCGEVAVVRMRGVEIYAMKILKNWEMVKGAEACFBEED	133			
QY	148	ILSRSTSPWIPOLQYAFQDKHLYLVMEYQPGDLSLNLRYEDQDENLIQVFLAELIL	207			
DB	134	VLVYGDRRWITNLHAFQDEKNLYIGDMMTLISKFVDHPIESMAKFIAMVIL	193			
QY	208	AVHSVHLGMGYVHRDIKPENILVDRTGHIKLVDFGSAKNSNNKNNVNAKLPITGPDYMAPE	267			
DB	194	AIDSLHRLGYVHRDKPDVNDVLLDMQGHIRLADFGSCLRLADGSAVSNVAVGTPDVISPE	253			
QY	268	VLTVMGDKGYGLDCDWWSGVGIYAYEMVYGRSPABGTSARTFNINNFQRLFKPPDD	327			
DB	254	ILFRAME-DGRGRYKGECDWLSGLICWYEMLYGTTPFYSERLVDITYGKINSHQMDLFPDD	312			
QY	328	P---KVSSDFDLILQSLCGQKERLKFEGLC---CHPFFSKIDNNIRNSPPPEVPTLKS	381			
DB	313	EDWVVESEAKLIQILICSSDVRFORNGLSDFQLHPFFEGIDWNTIRSNPPIVFEVSS	372			
QY	382	DDTSNFDPEKNSWVSSSPCQLSP-----SGFSGEELPFVFGFSYKALGILGRSESVSG	437			

Db 373 PEDTSNEDVDVCE--DFTTCETOPPRVLAFTGNHLPVFGFSYTHG-SLLSDARSUTDE 429  
Qy 438 LDSPAKTSMEKKLLIKS 455  
Db 430 IRAIAQRQCGDAELMEKS 447

RESULT 2  
T14039  
protein kinase (EC 2.7.1.37), myotonic dystrophy-associated - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2004  
C/Accession: T14039  
R;Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.  
Mol. Cell. Biol. 18, 130-140, 1998  
A;Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector  
A;Reference number: Z17862; MUID:98078670; PMID:9418861  
A;Accession: T14039  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1732 <LEU>  
A;Cross-references: UNIPROT:O54874; EMBL:AF021935; NID:g2736150; PID:g2736151; PIDN:AA00  
C;Genetics:  
A;Gene: MRCK  
A;Superfamily: protein kinase homology  
C;Keywords: ATP; phosphotransferase  
F;73-343/Domain: protein kinase homology <KIN>  
F;1013-1062/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 34.2%; Score 891; DB 2; Length 1732;  
Best Local Similarity 40.3%; Pred. No. 1.5e-32;  
Matches 183; Conservative 91; Mismatches 146; Indels 34; Gaps 8;

Qy 36 PFMTQOQMSPLREGILDALFVLFECSPALMKIKHVSFVRKYSDTIAELOELQPSAK 95  
Db 18 PAQTNGQC--FSVETLLDILICLVDCNNSPLREKNIILEWAKPFTSKVQMLHRE 75  
Qy 96 DFEVRSVGGCHFAEVQVREKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSP 155  
Db 76 DFEILKVIKRGAFGEVAVVKKNADKVFAMKILNKWELKRAETACFREERDVLVNGDSK 135  
Qy 156 WIPOLQAFODKNHLYVMEYQPGDLSLLNRYEDQDENLQFYLAELILAVHSVHLM 215  
Db 136 WITLHVAFODNNLYVMDYVGGDLTLTLSEFEDLPEDMARFYLAENVIADSVHQL 195  
Qy 216 GYVHRDIKPNILVDRTGHILKLVDFGSAAKNSKMNKYNAPLIGTPDYMAPEVLTVMNGD 275  
Db 196 HYVHRDIKPNILMDNMHGRILADFGSCLLMEDGTVOSSVAVGTPDYISPEILQAME-D 254  
Qy 276 GKGTGLDCDWWSGVYAYEMIGRSPFAGTSARTFNINMNFQRLKFPDD-PKVSSDF 334  
Db 255 GKGRYGECDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHKRFQFPPTQVTDVSENA 314  
Qy 335 LDLIQSLCCQKRLKPEGL---CCHPFFSKIDWNIRNSPPFPVPTLKSDDDTSNFDPEP 391  
Db 315 KDILRLRLCSREHLRGQNGIEDPKHAFGLWENIRNLEAPYIPDVSSPDSINFDVDDVLRNIE 374  
Qy 392 E---KNSWSSSPQCLSPSGFSGEELPFGVFSYKALGLGRS-----ESV 434  
Db 375 DDCLKNSSETMPPPP---THTAFSGHLLPFGVFTYTSSCVLSDRSLKRVAGTPTSLDLDMNV 431  
Qy 435 VSGLDSPAKTSMEKKL-----LIKSKELQDS 461  
Db 432 QRTLDNNLATEAYERRIKRLQEKLELTKLQES 465

RESULT 3  
T14050  
protein kinase (EC 2.7.1.37) beta, myotonic dystrophy-associated - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2004  
C/Accession: T14050

R;leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.  
Mol. Cell. Biol. 18, 130-140, 1998  
A;Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector  
A;Reference number: Z17862; MUID:98078670; PMID:9418861  
A;Accession: T14050  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1702 <LEU>  
A;Cross-references: UNIPROT:O54875; EMBL:AF021936; NID:g2736152; PID:g2736153; PIDN:AA00  
C;Genetics:  
A;Gene: MRCK-beta  
A;Superfamily: protein kinase homology  
C;Keywords: ATP; phosphotransferase  
F;74-342/Domain: protein kinase homology <KIN>  
F;1027-1076/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 33.9%; Score 883; DB 2; Length 1702;  
Best Local Similarity 40.5%; Pred. No. 3.4e-32;  
Matches 182; Conservative 90; Mismatches 139; Indels 38; Gaps 9;

Qy 44 SPLSREGILDALFVLFECSPALMKIKHVSFVRKYSDTIAELOELQPSAKDFEVRSLV 103  
Db 23 SLSVETLLDVLVCLVTECHSALRDKYVAEFLEWAKPFTQLVKDMLHREDFEIKVI 82  
Qy 104 GCGHFAEVQVREKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYA 163  
Db 83 GRGAFGEVAVVKMNTIRIYAMKILNKWELKRAETACFREERDVLVNGDCQWITALHYA 142  
Qy 164 FODKNHLYVMEYQPGDLSLLNRYEDQDENLQFYLAELILAVHSVHLMGYVHRDIK 223  
Db 143 FQDENLYLVMDYVGGDLTLTLSEFEDKLPEDMARFYLAENVIADSVHQLHYVHRDIK 202  
Qy 224 PENILVDRTGHILKLVDFGSAAKNSKMNKYNAPLIGTPDYMAPEVLTVMNGDGKGTGYGLD 283  
Db 203 PDNVLLDVNGHIRLADFGSCLMNDGTVOSSVAVGTPDYISPEILQAME-DGMGKYGE 261  
Qy 284 CDWWSGVYAYEMIGRSPFAGTSARTFNINMNFQRLKFPDD-PKVSSDFDLILQSL 342  
Db 262 CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHKRFQFPFHVTVDSSEAKDLIQLRI 321  
Qy 343 CGQKRLKPEGL---CCHPFFSKIDWNIRNSPPFPVPTLKSDDDTSNFDPEP---KNSW 396  
Db 322 CSRRRLGQNGIEDPKHAFGLWENIRNLEAPYIPDVSSPDSINFDVDDVLRNIE 381  
Qy 397 VSSSPQCLSP---SGPSGEELPFGVFSYKALGLGRS-----KAL---GILGRSESVVSGLD 439  
Db 382 I-----LPPGSHTGFGSLHLPFGFTFTTESCFSDRGLSKSMIQSNLTILTKDEDVQDRL 435  
Qy 440 SPAKTSMEKKL-----LIKSKELQDS 461  
Db 436 NSLQTEAYERRIRRLQEKLELTKLQES 464

RESULT 4  
T25539  
hypothetical protein C10H11.9 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T25539  
R;Dante, M.; Wamsley, P.  
submitted to the EMBL Data Library, February 1997  
A;Description: The sequence of C. elegans cosmid C10H11.  
A;Reference number: Z20047  
A;Status: preliminary;  
A;Accession: T25539  
A;Molecule type: DNA  
A;Residues: 1-1173 <DAN>  
A;Cross-references: UNIPROT:P92199; EMBL:U88311; PIDN:AA842348.1; GSPDB:GN00019; CBSP:C10  
C;Genetics:  
A;Gene: CBSP:C10H11.9  
A;Map position: 1



Db 379 ETFFI---PRAFGVQQLPFGVFTYYNRRYLSSANPDNRITSSNADKSLQESLQKTIYKL 435  
Qy 456 KE-----LQDS-QDKC 465  
Db 436 EEQLHNEWQLKDEMEQKC 453

RESULT 7  
B49364  
protein kinase (EC 2.7.1.37), myotonic dystrophy-associated - human  
N;Alternate names: myotonin protein kinase  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 16-Aug-2004  
C;Accession: B49364; S48681; A42101  
R;Shaw, D.J.; McCurrach, M.; Rundie, S.A.; Harley, H.G.; Crow, S.R.; Sohn, R.; Thirion,  
Genomics 18, 673-679, 1993  
A;Title: Genomic organization and transcriptional units at the myotonic dystrophy locus.  
A;Reference number: A49364; MUID:94140369; PMID:7905855  
A;Accession: B49364  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-624 <SHA>  
A;Cross-references: UNIPROT:Q09013; GB:L19268; NID:G307176; PIDN:AAA36206.1; PID:G307177  
R;Sasagawa, N.; Sorimachi, H.; Maruyama, K.; Arahata, K.; Ishiura, S.; Suzuki, K.  
FEBS Lett. 351, 22-26, 1994  
A;Title: Expression of a novel human myotonin protein kinase (MPK) cDNA clone which enc  
A;Reference number: S48681; MUID:94357271; PMID:8076686  
A;Accession: S48681  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-417, 'L', 419-468, 'P', 470-544, 'MAPRPLWASRWGQAPCTAATCCSLPGS', 'LGLAVRRFPCCS  
A;Cross-references: GB:S72893; NID:G633864; PIDN:AB31800.1; PID:G633865  
R;Brook, J.D.; McCurrach, M.E.; Harley, H.G.; Buckler, A.J.; Church, D.; Aburatani, H.;  
S.; Davies, J.; Sheldbourne, P.; Buxton, J.; Jones, C.; Juvonen, V.; Johnson, K.; Harper,  
Cell 68, 799-808, 1992  
A;Title: Molecular basis of myotonic dystrophy: expansion of a trinucleotide (CTG) repea  
A;Reference number: A42101; MUID:92154692; PMID:1310900  
A;Accession: A42101  
A;Molecule type: mRNA  
A;Residues: 'PFGQVRGLLAVGGA', 57-550, 'WLWASRWGQA', 564-624 <BRO>  
A;Cross-references: GB:M94203; GB:M91465; NID:G186755; PIDN:AAA64884.1; PID:G186756  
A;Note: sequence extracted from NCBI backbone (NCBIN:82640, NCBI:82641)  
C;Genetics:  
A;Gene: GDB:DM  
A;Cross-references: GDB:119097; OMIM:160900  
A;Map position: 19q13.2-19q13.3  
C;Superfamily: protein kinase homology  
C;Keywords: ATP; phosphotransferase  
F;69-339/Domain: protein kinase homology <KIN>  
F;77-85/Region: protein kinase ATP-binding motif

Query Match 33.2%; Score 863; DB 2; Length 624;  
Best Local Similarity 40.8%; Pred. No. 1e-31;  
Matches 179; Conservative 88; Mismatches 154; Indels 18; Gaps 7;

Qy 46 LSREGILDALFVLFEECSQPALMKIKHVSFVRKYSDTIAELOLQPSAKDFEVSILVC 105  
Db 20 LGLEPLDULLGVLQELGASLQADKYADVLQWAPFVVRLEKVRQLQRDDFFILKVI 79  
Qy 106 GHFAEQVVRKATGDIYAMKVMKKALLAQEQVSFFEEERNILSRSTSIPWQLQYAFQ 165  
Db 80 GAFSEVAVVRKMTQGVYAMKINMKDMLKRGVSCFEEERDVLVNGDRWITQLHFAFQ 139  
Qy 166 DKHLYLVMEYQPGDLSLLNRYEDQLDENLQFYLAELILAVHSHLMGVYHRIKPE 225  
Db 140 DENLYLVMEYQPGDLSLLNRYEDQLDENLQFYLAELILAVHSHLMGVYHRIKPE 225  
Qy 226 NILVDRTGHIKLVDFGSAKKMNMKNVNAKLPIGTDPDYMAPEVL-TVMNGDGKGTGLDC 284  
Db 200 NILDCRGHRLADFGSLKLRADGTVRSIVAGTDPDYSPEILQAVGGPGTGTGPEC 259  
Qy 285 DWSVGVYAYEMTYGRSPFAEGTSARTFNNIMNQRFLKFP-DDPKVSSDFDLIQSLLC 343

Db 260 DWALGVFAYEMYGTPTFYADSTAYTGKIVHYKEHLSLPLVDEGVPEARDFIQLLC 319  
Qy 344 GQKERLKFEQ---LCCHPFFSKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSS 400  
Db 320 PPETRLRGAGGDFRTHPFFFGLDWDGLRDSVPFPTDFEGATDTCNFDLVEDGLTAMET 379  
Qy 401 PCOLSPSGSGEELPFVGFSGYSKALGILGRSESVWSGLDSPAKTSSMEKKLL---LKSKE 457  
Db 380 LSDIREGAPLGVHLPFVGSYS---CMALRDSVEFG---PTPMEVEASQLLEPHVQAPS 432  
Qy 458 LQDS---QDKCHKVFISAA 473  
Db 433 LEPSVSPQDETAEVAVPAA 451

RESULT 8  
S70633  
serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - bovine  
N;Alternate names: Rho-associated protein kinase  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 16-Aug-2004  
C;Accession: S70633; S77694  
R;Matsui, T.; Amano, M.; Yamamoto, T.; Chihara, K.; Nakafuku, M.; Ito, M.; Nakano, T.; O  
EMBO J. 15, 2208-2216, 1996  
A;Title: Rho-associated kinase, a novel serine/threonine kinase, as a putative target fo  
A;Reference number: S70633; MUID:96208507; PMID:8641286  
A;Accession: S70633  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1388 <MAT1>  
A;Cross-references: UNIPROT:Q28021; EMBL:U36909; NID:G1326077; PIDN:AAC48567.1; PID:G1326  
A;Accession: S77694  
A;Molecule type: protein  
A;Residues: 1-18;30-34;36-44;58-64;133-140;248-252;291-295;297-305;327-347;350-360;366-3  
-1070 <MAT2>  
C;Superfamily: protein kinase C zinc-binding repeat homology; protein kinase homology  
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F;90-354/Domain: protein kinase homology <KIN>  
F;98-106/Region: protein kinase ATP-binding motif  
F;1261-1315/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 33.1%; Score 860.5; DB 2; Length 1388;  
Best Local Similarity 39.5%; Pred. No. 2.8e-31;  
Matches 183; Conservative 98; Mismatches 147; Indels 35; Gaps 11;

Qy 15 GAABPIAN---RASRLNLFQCKPPMTQQQSPJLSREGILDALFVLFEECSQPALMKIK 71  
Db 12 GAPEAVSGDGAGASR-----QRKLEALIRDRPSINVESLDDGLNPLVLDLDFPALRKNNK 66  
Qy 72 HVSNFVRKYSDTIAELOLQPSAKDFEVSILVCQGHFAEVQVVRKATGDIYAMKVMKK 131  
Db 67 NIDNFLNRYEKIVKKIRGLQMKAEYDVVVKVIGRGAFGEVQLVRHKASQKVYAMKULSKP 126  
Qy 132 ALLAQOVQVFFEEERNILSRSTSIPWQLQYAFQDKNHLVLMVEYQPGDLSLLNRYED 191  
Db 127 EMIKRSDSAFFWEERDIFAFANSPVVQLFCFAQDDKYLVMWYMWPGDGLVNLMSNYD- 185  
Qy 192 QLDENLIQYLAELILAVHSHLMGVYHRIKPEINILVDRTGHIKLVDFGSAKKMNSKM 251  
Db 186 -VPEKWAQYTTAEVVLALDAIHSMLIHRDVPDNNMLDKHGLKLADFGTCMKMDETGM 244  
Qy 252 VNAKLPIGTDPDYMAPEVLTVMNGDGKGTGLDCDWSVGVYAYEMTYGRSPFAEGTSART 311  
Db 245 VHCDTAVGPDYISPEVLKSCQGGD--GYGRSCDWSVGVFLPEMLVGTDPFYADSLVGT 302  
Qy 312 FNNIMNQRFLKFPDDPKVSSDFDLIQSLLCQCKERLKFEQ---LCCHPFFSKIDWN-- 366  
Db 303 YSKIMDKNLSLCPEDAELISKHAKNLICAFLTRVRLGRNGVVEIKQHPFFKQDNQWWD 362  
Qy 367 NTRNSPPPPVPTLKSDDDTSNFDPEKNSW-VSSSPCQLSPSGFSGEELPFVGFYSKAL 425  
Db 363 NIRETAAPVVPVPELSSDISSNFDIEDDKGDVETFFI---PKAFVGNQLPFIQFTTYREN 419

## RESULT 13

S60966  
Probable protein kinase YNL161w (EC 2.7.1.-) - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: hypothetical protein N1727  
C:Species: *Saccharomyces cerevisiae*  
C/Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 16-Aug-2004  
C/Accession: S60966; S63113; S63813  
R:Naar, F.; Becam, A.M.; Herbert, C.J.  
submitted to the EMBL Data Library, October 1995  
A:Description: The sequence of 36.8 kb from the left arm of chromosome XIV reveals  
tonic dystrophy kinase.  
A:Reference number: S60958  
A:Accession: S60966  
A:Molecule type: DNA  
A:Residues: 1-756 <NAS>  
A:Cross-references: UNIPROT:P53894; EMBL:X92517; NID:G1050783; PIDN:CAA63278.1  
R:Naar, F.; Becam, A.M.; Herbert, C.  
submitted to the Protein Sequence Database, April 1996  
A:Reference number: S62967

A:Naar, F.; Becam, A.M.; Heribert, C.J.  
 submitted to the Protein Sequence Database, April 1996  
 A:Reference number: S62967  
 A:Accession: S63113  
 A:Molecule type: DNA  
 A:Residues: 1-756 <NAW>  
 A:Cross-references: EMBL:Z71437; NID:G1302127; PIDN:CAA96048.1; PID:G339962; P  
 A:Experimental source: Strain S288C  
 A:Naar, F.; Becam, A.M.; Heribert, C.J.  
 Yeast 12, 169-175, 1996  
 A:Title: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 2  
 dysophy kinase.  
 A:Reference number: S63805; MUID:96287653; PMID:8686380

A: Gene: SGD: YNL161W  
A: Cross-references: SGD: S0005105  
A: Map position: 14L  
A: Note: YNL161W  
C: Superfamily: protein kinase homology  
C: Keywords: ATP; phosphotransferase  
F: 350-672/Domain: protein kinase homology <KIN>  
F: 358-366/Region: protein kinase ATP-binding motif

Query Match	27.1%	Score 704;	DB 2;	Length 756;
Best Local Similarity	32.7%	Pred. NO. 1.4e-24;		
Matches 163;	Conservative	82;	Mismatches 159;	Indels 94;
				Gaps 10





Db	268	IWLTSSKDXMATWKXRRVWAYSTVGTDPYIAPEIF-LQOG-----YQODCDWWSLCAI	321
Qy	293	AYEMYGRSPFAEGTSARTFNNINMFORFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFE	352
Db	322	MFECLIGWPPFCSENSHETYRKIIINWRETLTFPNDIHLSTIARDLMDRLMTDSEHRLGRG	381
Qy	353	G---LCCHPFSKIDWNNIRNSPPFPVPTLKSDDDTSNF--DEPEK--NSWVSSSPCQLS	405
Db	382	GAIEIMQHPPFTGIDWDHIHRETAAPFIPNLKSITDTHYFPVDELEQVPEQVTPQOPASVD	441
Qy	406	PSGFSGEELPFVGFYSK	423
Db	442	POTLEQTNLAFGLGYTKK	459

Search completed: March 18, 2005, 15:40:47  
 Job time : 45 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:21:39 ; Search time 174 Seconds  
(without alignments)  
1104.712 Million cell updates/sec

Title: US-10-724-594-2

Perfect score: 2602

Sequence: 1 MLKFKYGARNPLDAGAAEPI.....CSRILPSVYAKSGARGCWL 497

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2602	100.0	497	6	ABU10126 Novel hum
2	2602	100.0	497	7	Aae39504 Human kin
3	2602	100.0	497	8	Ado40592 Human kin
4	2597	99.8	497	6	Abp97687 Amino aci
5	2589	99.5	497	5	Aae16261 Human kin
6	2589	99.5	497	6	Abu10127 Variant n
7	2582	99.2	495	6	Abp97681 Amino aci
8	2440	93.8	620	8	Adn62809 Human NOV
9	2440	93.8	623	6	Ada05644 Human NOV
10	2440	93.8	1958	5	Abb81928 Human kin
11	2440	93.8	2054	5	Abb81927 Human kin
12	2440	93.8	2054	5	Aae24150 Human kin
13	2440	93.8	2054	6	Aao26959 Human CRI
14	2430	93.4	2053	5	Aae24079 Human MDP
15	2430	93.4	2053	7	Adf60994 Pain asso
16	2430	93.4	2053	8	Adq89100 Human uro
17	2418.5	92.9	2053	4	Aau03501 Human pro
18	2418.5	92.9	2055	8	Adj96610 Human cit
19	2412.5	92.7	2053	5	Abg78363 RHO/RAC-1
20	2412.5	92.7	2053	6	Ada05642 Human NOV
21	2412.5	92.7	2053	8	Adn63228 Human NOV
22	2412.5	92.7	2053	8	Adn62807 Human NOV
23	2412.5	92.7	2066	5	Abg78362 Human pro
24	2412.5	92.7	2066	6	Ada05654 Human NOV
25	2400.5	92.3	2066	8	Adn62819 Human NOV

26	2271.5	87.3	494	6	Abp97682
27	2271.5	87.3	494	8	Ado40594
28	2172.5	83.5	2055	6	Abp97683
29	2172.5	83.5	2055	6	Aao26960
30	1652	63.5	319	7	Adn62730
31	1627	62.5	349	4	Abg15566
32	1284	49.3	257	7	Adj79947
33	1180	45.3	251	7	Adj79949
34	1177	45.2	251	7	Adj79950
35	932.5	35.8	1565	8	Adp47967
36	929	35.7	475	5	Aae24131
37	929	35.7	1197	6	Abj37881
38	929	35.7	1247	6	Abj37882
39	929	35.7	1551	8	Adi40850
40	929	35.7	1553	7	Adc99064
41	929	35.7	1569	8	Adf95102
42	929	35.7	1572	5	Aae19162
43	929	35.7	1572	8	Adj96611
44	929	35.7	1572	8	Adq15094
45	926	35.6	1648	8	Adf95100

ALIGNMENTS

RESULT 1

ABU10126

ID ABU10126 standard; protein; 497 AA.

XX AC ABU10126;

XX DT 11-AUG-2003 (first entry)

XX DE Novel human kinase.

XX KW Human; enzyme; gene therapy; kinase; antisense.

XX OS Homo sapiens.

XX PN US2003022340-A1.

XX PD 30-JAN-2003.

XX PF 11-SEP-2002; 2002US-00238709.

XX PR 13-MAR-2001; 2001US-00804471.

XX PA (APPL-) APPLERA CORP.

XX PI Webster M, Yan C, Di Francesco V, Beasley EM;

XX DR WPI; 2003-438978/41.

XX DR N-PSDB; ACA61394.

XX PT New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression.

XX PS Claim 1; Fig 2; 207pp; English.

XX CC The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are useful as hybridisation probes, in constructing vectors, host cells or transgenic animals expressing all or a part of the nucleic acid, for

CC monitoring the effectiveness of modulating compounds on the expression or  
 CC activity of the transporter gene in clinical trials or in treatment  
 CC regimen, in gene therapy and as antisense constructs to control  
 CC transporter gene expression in cells, tissue and organisms. The present  
 CC sequence represents the amino acid sequence of a novel human kinase  
 XX  
 SQ Sequence 497 AA;

Query Match 100.0%; Score 2602; DB 6; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-254;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARPLDGAAGAAETANRASRLNLFQGGPPMTQQMSPLSREGILDALFVLF 60  
 Db 1 MLKFKYGARPLDGAAGAAETANRASRLNLFQGGPPMTQQMSPLSREGILDALFVLF 60  
 Qy 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVSRLVGCCHFAEVQVREKATG 120  
 Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVSRLVGCCHFAEVQVREKATG 120  
 Qy 121 DIYAMKMKKALLAQOVFFBEERNILSRSTSPWIPQLOYAFQDKXHLVLYVMEYQPG 180  
 Db 121 DIYAMKMKKALLAQOVFFBEERNILSRSTSPWIPQLOYAFQDKXHLVLYVMEYQPG 180  
 Qy 181 DLLSLNRYEDQDENLIQYLAELILAVHSVHLMGVVHRDIKPENILVDRTGHIKLVD 240  
 Db 181 DLLSLNRYEDQDENLIQYLAELILAVHSVHLMGVVHRDIKPENILVDRTGHIKLVD 240  
 Qy 241 GSAAKMNSKVNNAKLPIGTDPYMAPEVLTVMGDGGKTYGLDCDWMVSGVIAIYMIYGR 300  
 Db 241 GSAAKMNSKVNNAKLPIGTDPYMAPEVLTVMGDGGKTYGLDCDWMVSGVIAIYMIYGR 300  
 Qy 301 SPFAEGTSARTFNIMNFQRLKFPDPKYSDFDLDIQSLCGQKRLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNIMNFQRLKFPDPKYSDFDLDIQSLCGQKRLKFEGLCCHPFF 360  
 Qy 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPFCOLSPGSGEELPFVGF 420  
 Db 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPFCOLSPGSGEELPFVGF 420  
 Qy 421 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFTISAAGLIPCSR 480  
 Db 421 YSKALGILGRSESVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKVFTISAAGLIPCSR 480  
 Qy 481 ILPSVYAKSGARGRCWL 497  
 Db 481 ILPSVYAKSGARGRCWL 497

RESULT 2  
 AAE39504  
 ID AAE39504 standard; protein; 497 AA.  
 XX  
 AC AAE39504;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human kinase protein.  
 XX  
 KW Human; kinase protein; diagnostic; therapeutic; immune response; enzyme;  
 KW pharmacogenomic; tissue typing; gene therapy; chromosome 12; transgenic.  
 XX  
 OS Homo sapiens.  
 XX

Key Location/Qualifiers  
 FH Modified-site 50..55  
 FT /note= "N-myristoylation site"  
 FT Modified-site 78..81  
 FT /note= "cAMP and cGMP dependent protein kinase  
 phosphorylation site"  
 FT Modified-site 83..86  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site 93..96

FT /note= "Caesin kinase II phosphorylation site"  
 FT 93..95  
 FT /note= "Protein kinase C phosphorylation site"  
 FT 103..126  
 FT /note= "Protein kinase ATP-binding region signature"  
 FT 140..143  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT 197..217  
 FT /note= "Helix I"  
 FT 217..229  
 FT /note= "Serine/Threonine protein kinase active-site  
 signature"  
 FT 248..250  
 FT /note= "Protein kinase C phosphorylation site"  
 FT 308..310  
 FT /note= "Protein kinase C phosphorylation site"  
 FT 361..364  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT 365  
 FT /note= "This residue changes to Cys during single  
 nucleotide polymorphism (SNP)"  
 FT 378..380  
 FT /note= "Protein kinase C phosphorylation site"  
 FT 381..384  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT 386..389  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT 410..413  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT 436..439  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT 445..448  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT 467..487  
 FT /note= "Helix II"  
 FT 474..479  
 FT /note= "N-myristoylation site"  
 FT 489..494  
 FT /note= "N-myristoylation site"  
 FT 490..492  
 FT /note= "Protein kinase C phosphorylation site"  
 FT  
 PN US2002132322-A1.  
 PD 19-SEP-2002.  
 XX  
 PF 13-MAR-2001; 2001US-00804471.  
 XX  
 PR 13-MAR-2001; 2001US-00804471.  
 XX  
 PA (WEBS/) WEBSTER M.  
 PA (YANC/) YAN C.  
 PA (DFRA/) DI FRANCESCO V.  
 PA (BEAS/) BEASLEY E M.  
 XX  
 PI Webster M, Yan C, Di Francesco V, Beasley EM;  
 XX  
 XX WPI; 2003-587480/65.  
 DR N-PSDB; AAD59937, AAD59938.  
 DR  
 XX New isolated human kinase proteins, useful as models for developing human  
 PT therapeutic targets, or for treating a disorder associated with an  
 PT absence of, inappropriate or unwanted expression of the protein, e.g.  
 PT cancer.  
 FT  
 XX Claim 1; Fig 2; Opp; English.  
 PS  
 CC The present invention relates to human kinase proteins and nucleic acids  
 CC encoding them all of which are useful in the development of human  
 CC therapeutics and diagnostic composition and methods. The invention is  
 CC useful as models for the development of human therapeutic targets, aid in  
 CC the identification of therapeutic proteins and serve as targets for the  
 CC development of human therapeutic agents. The invention is also useful in

CC drug screening assays, in assays to determine the biological activity of  
CC the protein, to raise antibodies and to elicit another immune response.  
CC The antibodies are useful in pharmacogenomic analysis, for inhibiting  
CC protein function and for tissue typing. The transgenic animals are useful  
CC for studying the function of kinase protein, identifying and evaluating  
CC modulators of kinase protein activity. The invention is also used in gene  
CC therapy. The present sequence is the human kinase protein. The human  
CC kinase gene is located on chromosome 12  
XX  
SQ Sequence 497 AA;

Query Match 100.0%; Score 2602; DB 7; Length 497;  
Best Local Similarity 100.0%; Pred. No. 2.1e-254;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAETANRASRLNLFQFGKPPFTMQQMSPLSREGILDALFVLPF 60  
Db 1 MLKFKYGARNPLDAGAAETANRASRLNLFQFGKPPFTMQQMSPLSREGILDALFVLPF 60

Qy 61 ECSQPALMKIKHVSFNFRKYSYDTIABELOELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120  
Db 61 ECSQPALMKIKHVSFNFRKYSYDTIABELOELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120

Qy 121 DIYAMQVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLOYAFQDNHLYLYMVEYQPG 180  
Db 121 DIYAMQVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLOYAFQDNHLYLYMVEYQPG 180

Qy 181 DLLSLNRYEDQDENLIQFYLAELIIVHSHVLMGVVHRDIKPNILVDRTGHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELIIVHSHVLMGVVHRDIKPNILVDRTGHIKLVDF 240

Qy 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMSVGVIAIYMIYGR 300  
Db 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMSVGVIAIYMIYGR 300

Qy 301 SPPAEGTSARTFNINNFQRLKPPDDPKVSSDFLDLIQSLCGKRLKFEGLCCHPFF 360  
Db 301 SPPAEGTSARTFNINNFQRLKPPDDPKVSSDFLDLIQSLCGKRLKFEGLCCHPFF 360

Qy 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCOLSPGSGBELPFVGF 420  
Db 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCOLSPGSGBELPFVGF 420

Qy 421 YSKALGILGRSESVVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKVFTISAAGLLPCSR 480  
Db 421 YSKALGILGRSESVVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKVFTISAAGLLPCSR 480

Qy 481 ILPSVYAKSGARGCWL 497  
Db 481 ILPSVYAKSGARGCWL 497

RESULT 3  
ADO40592  
ID ADO40592 standard; protein; 497 AA.  
XX  
XX  
AC ADO40592;  
XX  
XX 29-JUL-2004 (first entry)  
DE Human kinase protein.  
XX Kinase; rho/rac-interacting citron kinase; drug screening;  
XX Kinase related disorder; human; enzyme.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 50..55  
FT Modified-site /note= "N-myristoylation site"  
FT Modified-site 78..81  
FT /note= "cAMP and cGMP dependent protein kinase  
FT phosphorylation site"

FT Modified-site 93..86  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 93..96  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 93..95  
FT /note= "Protein kinase C phosphorylation site"  
FT Binding-site 103..126  
FT /note= "Protein kinase ATP-binding region signature"  
FT Modified-site 140..143  
FT /note= "Casein kinase II phosphorylation site"  
FT Region 197..217  
FT /note= "Helix 1"  
FT Active-site 217..229  
FT /note= "Serine/Threonine protein kinase active-site  
FT signature"  
FT Modified-site 248..250  
FT /note= "Protein kinase C phosphorylation site"  
FT Modified-site 308..310  
FT /note= "Protein kinase C phosphorylation site"  
FT Modified-site 361..364  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 378..380  
FT /note= "Protein kinase C phosphorylation site"  
FT Modified-site 381..384  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 386..389  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 410..413  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 436..439  
FT /note= "Casein kinase II phosphorylation site"  
FT Modified-site 445..448  
FT /note= "Casein kinase II phosphorylation site"  
FT Region 467..487  
FT /note= "Helix 2"  
FT Modified-site 474..479  
FT /note= "N-myristoylation site"  
FT Modified-site 489..494  
FT /note= "N-myristoylation site"  
FT Modified-site 490..492  
FT /note= "Protein kinase C phosphorylation site"  
XX  
XX US2004091993-A1.  
XX  
XX 13-MAY-2004.  
XX  
XX 02-DEC-2003; 2003US-00724594.  
XX  
XX 13-MAR-2001; 2001US-00804471.  
XX 11-SEP-2002; 2002US-00238709.  
XX  
XX (APPL-) APPLERA CORP.  
XX  
XX Webster M, Yan C, Di Francesco V, Beasley EM;  
XX  
XX WPI; 2004-374957/35.  
XX N-PSDB; ADO40591, ADO40593.  
XX  
XX New isolated human kinase proteins and nucleic acids, useful for  
XX developing human therapeutic targets, identifying therapeutic proteins or  
XX serve as targets for the development of human therapeutic agents that  
XX modulate kinase activity.  
XX  
XX Claim 1; SEQ ID NO 2; 207pp; English.

CC The present invention provides a kinase polypeptide and its encoding  
CC polynucleotide. The polypeptide and polynucleotide of the invention are  
CC useful as models for the development of human therapeutic targets, aid in  
CC the identification of therapeutic proteins and serve as targets for the  
CC development of human therapeutic agents that modulate kinase activity in  
CC cells and tissues that express the kinase. The invention is also useful  
CC for biological assays related to kinases, in drug screening assays, for  
CC treating disorders characterized by an absence of inappropriate and

CC unwanted expression of the protein. The present sequence is the human  
 CC kinase protein.  
 XX  
 SQ Sequence 497 AA;

Query Match 100.0%; Score 2602; DB 8; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-254;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQKPPMTQQQMSPLSREGILDALFVLF 60  
 Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQKPPMTQQQMSPLSREGILDALFVLF 60

Qy 61 ECSOPALMKIKHVSFVRKYSDTIAELOELQPSAKDFEVSILVCGHFAEVQVREKATG 120  
 Db 61 ECSOPALMKIKHVSFVRKYSDTIAELOELQPSAKDFEVSILVCGHFAEVQVREKATG 120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLILVMEYQPGG 180  
 Db 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLILVMEYQPGG 180

Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240

Qy 241 GSAKMNNSKMNWNAKLPIGTPTYMAPEVLTVMNGDGKGTGLDQDMSVGVIAEYMIYGR 300  
 Db 241 GSAKMNNSKMNWNAKLPIGTPTYMAPEVLTVMNGDGKGTGLDQDMSVGVIAEYMIYGR 300

Qy 301 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIQSLLCQKXERLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIQSLLCQKXERLKFEGLCCHPFF 360

Qy 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGSGBELPFVFGFS 420  
 Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGSGBELPFVFGFS 420

Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy 481 ILPSVYAKSGARGCWL 497  
 Db 481 ILPSVYAKSGARGCWL 497

RESULT 4  
 ABP97687  
 ID ABP97687 standard; protein; 497 AA.  
 XX  
 AC ABP97687;  
 XX  
 DT 16-MAY-2003 (first entry)  
 XX  
 DE Amino acid sequence of citron rho/rac-interacting kinase-short kinase.  
 XX  
 KW Human; citron rho/rac-interacting kinase-short kinase; obesity;  
 KW chronic obstructive pulmonary disease; hypertension; diabetes;  
 KW coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;  
 KW gout; osteoarthritis; sleep apnea; cancer; thrombotic disease;  
 KW polycystic ovarian syndrome; fertility; depression.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02003004629-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 01-JUL-2002; 2002WO-EP007229.  
 XX  
 PR 02-JUL-2001; 2001US-0301853P.  
 PR 10-DEC-2001; 2001US-0337130P.  
 PR 25-APR-2002; 2002US-0375015P.

XX (FARB ) BAYER AG.  
 PA  
 XX Zhu Z;  
 PI  
 XX  
 DR WPI; 2003-221595/21.  
 DR N-PSDB; ABZ68726.  
 XX  
 PT New human citron rho/rac-interacting kinase-short kinase polypeptide and  
 PT polynucleotide for preventing or treating diseases associated with the  
 PT polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary  
 PT disease.  
 XX  
 PS Claim 1; Fig 19; 145pp; English.  
 XX  
 CC The present sequence represents a human citron rho/rac-interacting kinase  
 CC -short kinase polypeptide. The polynucleotide and polypeptide of the  
 CC invention are useful in preventing, ameliorating, or treating diseases  
 CC associated with the polypeptide dysfunction. The expression vector or the  
 CC reagent is useful in the preparation of a medicament for modulating the  
 CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
 CC disease, such as obesity or chronic obstructive pulmonary disease. These  
 CC may also be used for treating obesity/ overweight-associated  
 CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
 CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
 CC apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced  
 CC fertility, and depression  
 XX  
 SQ Sequence 497 AA;

Query Match 99.8%; Score 2597; DB 6; Length 497;  
 Best Local Similarity 99.8%; Pred. No. 6.9e-254;  
 Matches 496; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQKPPMTQQQMSPLSREGILDALFVLF 60  
 Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQKPPMTQQQMSPLSREGILDALFVLF 60

Qy 61 ECSOPALMKIKHVSFVRKYSDTIAELOELQPSAKDFEVSILVCGHFAEVQVREKATG 120  
 Db 61 ECSOPALMKIKHVSFVRKYSDTIAELOELQPSAKDFEVSILVCGHFAEVQVREKATG 120

Qy 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLILVMEYQPGG 180  
 Db 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLILVMEYQPGG 180

Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSHVLMGVVHRDIKPENILVDRTGHIKLVDF 240

Qy 241 GSAKMNNSKMNWNAKLPIGTPTYMAPEVLTVMNGDGKGTGLDQDMSVGVIAEYMIYGR 300  
 Db 241 GSAKMNNSKMNWNAKLPIGTPTYMAPEVLTVMNGDGKGTGLDQDMSVGVIAEYMIYGR 300

Qy 301 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIQSLLCQKXERLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIQSLLCQKXERLKFEGLCCHPFF 360

Qy 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGSGBELPFVFGFS 420  
 Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSSPCQLSPGSGSGBELPFVFGFS 420

Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480

Qy 481 ILPSVYAKSGARGCWL 497  
 Db 481 ILPSVYAKSGARGCWL 497

RESULT 5  
 AAE16261

ID AAE16261 standard; protein; 497 AA.  
 AC AAE16261;  
 XX  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human kinase PKIN-7 protein.  
 XX  
 KW Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis;  
 KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;  
 KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;  
 KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;  
 KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis;  
 KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;  
 KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;  
 KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;  
 KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;  
 KW congestive heart failure; ischaemic heart disease; lung tumour; gout;  
 KW fatty liver; Niemann-Pick's disease; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Location/Qualifiers  
 FT Domain :  
 FT 86..124 /label= Protein\_kinase\_domain  
 FT 96..153 /label= Protein\_kinase\_domain  
 FT 97..360 /label= Protein\_kinase\_domain  
 FT /note= "Eukaryotic protein kinase domain"  
 FT 98..241 /label= Protein\_kinase\_domain  
 FT 99..349 /label= Protein\_kinase\_domain  
 FT 101..241 /label= Protein\_kinase\_domain  
 FT 102..241 /label= Protein\_kinase\_domain  
 FT 249..349 /label= Protein\_kinase\_domain  
 FT 258..445 /label= Protein\_kinase\_domain  
 FT 258..349 /label= Protein\_kinase\_domain  
 FT 361..390 /label= Protein\_kinase\_domain  
 FT /note= "Protein kinase C terminal domain"  
 XX  
 WO200196547-A2.  
 XX  
 XX 20-DEC-2001.  
 XX  
 XX 14-JUN-2001; 2001WO-US019444.  
 XX  
 XX 15-JUN-2000; 2000US-0212073P.  
 XX 23-JUN-2000; 2000US-0213467P.  
 XX 30-JUN-2000; 2000US-0215651P.  
 XX 07-JUL-2000; 2000US-0216605P.  
 XX 13-JUL-2000; 2000US-0218372P.  
 XX 25-AUG-2000; 2000US-0228056P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;  
 PI Gandhi AR, Tribouley CM, Walla NK, Yao MG, Lu DM, Greenwald SR;  
 PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;  
 PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;  
 PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;  
 PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;  
 XX  
 XX WPI: 2002-090207/12.  
 DR N-PSDB; AAD26454.  
 XX  
 XX New polypeptides, useful for diagnosing, treating or preventing disorders  
 PT of growth and development, cardiovascular and lipid, and diseases such as

cancer, comprise human kinase polypeptides.  
 Claim 1; Page 146-147; 197pp; English.  
 XX  
 XX The invention relates to human kinase PKIN proteins and their  
 CC corresponding cDNAs. A composition containing PKIN agonist is useful for  
 CC treating a disease or condition associated with decreased expression of  
 CC PKIN and a composition comprising PKIN antagonist is useful for treating  
 CC a disease or condition associated with overexpression of PKIN. The  
 CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,  
 CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder  
 CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,  
 CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,  
 CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes  
 CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,  
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Renter's syndrome,  
 CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,  
 CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)  
 CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts; cardio  
 CC vascular disease (arteriovenous fistula, hypertension, vasculitis,  
 CC aneurysms, congestive heart failure, angina pectoris, myocarditis,  
 CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid  
 CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,  
 CC hypercholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity  
 CC of a test compound and in gene therapy. The present sequence is human  
 CC PKIN-7 protein  
 XX  
 SQ Sequence 497 AA;  
 Query Match 99.5%; Score 2589; DB 5; Length 497;  
 Best Local Similarity 99.6%; Pred. No. 4.5e-253;  
 Matches 495; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLF 60  
 DB 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSREGILDALFVLF 60  
 QY 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
 DB 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
 QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPGG 180  
 DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPGG 180  
 QY 181 DLLSLNRYEDQDENLIFOYLAELILAVHSHVLMGYVHRDIPENILVDRTGHIKLVD 240  
 DB 181 DLLSLNRYEDQDENLIFOYLAELILAVHSHVLMGYVHRDIPENILVDRTGHIKLVD 240  
 QY 241 GSAAKMNSNMKNYNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMVSGVIAYEIMYGR 300  
 DB 241 GSAAKMNSNMKNYNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMVSGVIAYEIMYGR 300  
 QY 301 SPFAECTSARTNNIMNFORFLKFPDDPKVSDFDLDLIQSLCGKXERLKFEGLCCHPFF 360  
 DB 301 SPFAECTSARTNNIMNFORFLKFPDDPKVSDFDLDLIQSLCGKXERLKFEGLCCHPFF 360  
 QY 361 SKIDWNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGEELPVPFGS 420  
 DB 361 SKIDWNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGEELPVPFGS 420  
 QY 421 YSKALGILGRSSVSGLDSPAKTSMKKLTIKSKELQDSODKCHKVFTISAAGLLPCSR 480  
 DB 421 YSKALGILGRSSVSGLDSPAKTSMKKLTIKSKELQDSODKCHKVFTISAAGLLPCSR 480  
 QY 481 ILPSVYAKGSARGRCWL 497  
 DB 481 ILPSVYAKGSARGRCWL 497  
 RESULT 6  
 ABU10127

```

ID  ABU10127 standard; protein; 497 AA.
XX
AC  ABU10127;
XX
DT  11-AUG-2003 (first entry)
XX
DE  Variant novel human kinase.
XX
KW  Human; enzyme; gene therapy; kinase; antisense.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  Misc-difference 365
FT  /note= "Wild-type Trp substituted by Cys as a result of a
FT  single nucleotide polymorphism"
XX
XX  US2003022340-A1.
XX
XX  30-JAN-2003.
XX
XX  11-SEP-2002; 2002US-00238709.
XX
XX  13-MAR-2001; 2001US-00804471.
XX
XX  (APPL-) APPLERA CORP.
XX
XX  Webster M, Yan C, Di Francesco V, Beasley EM;
XX  WPI; 2003-438978/41.
XX
XX  New human kinase peptides useful as models or targets for the development
XX  of therapeutic agents that modulate kinase activity, for eliciting immune
XX  response, and in identifying compounds that modulate kinase activity or
XX  expression.
XX
XX  Disclosure; Page; 207pp; English.
XX
XX  The invention relates to a novel isolated human kinase. The kinase
XX  peptides and nucleic acids are useful as models for the development of
XX  human therapeutic targets, in the identification of therapeutic proteins,
XX  and serve as targets for the development of human therapeutic agents that
XX  modulate kinase activity in cells and tissues that express the kinase.
XX  The proteins can be used to raise or to elicit another immune response,
XX  as a reagent in assays designed to determine the levels of the protein in
XX  biological fluids, as markers for tissue in which the corresponding
XX  protein is preferentially expressed, in the identification of modulators
XX  of the peptides and in pharmacogenomic analysis. The nucleic acids are
XX  useful as hybridisation probes, in constructing vectors, host cells or
XX  transgenic animals expressing all or a part of the nucleic acid, for
XX  monitoring the effectiveness of modulating compounds on the expression or
XX  activity of the transporter gene in clinical trials or in treatment
XX  regimen, in gene therapy and as antisense constructs to control
XX  transporter gene expression in cells, tissue and organisms. The present
XX  sequence represents the amino acid sequence of a variant novel human
XX  kinase. Note: The present sequence is not shown in the specification but
XX  was created by the indexer using the information given in figure 3
XX
XX  Sequence 497 AA;
XX
Query Match          99.5%; Score 2589; DB 6; Length 497;
Best Local Similarity 99.8%; Pred. No. 4.5e-253;
Matches 496; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY  1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQCKPFPMTQQMSPLSRREGILDALFVLE 60
DB  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQCKPFPMTQQMSPLSRREGILDALFVLE 60
QY  61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHGEAEVQVVRKATG 120
DB  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHGEAEVQVVRKATG 120
QY  121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDNHLYLWMEYQPGG 180

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XX New NOVX polypeptides and nucleic acids, useful for diagnosing,  
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,  
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX Claim 1; Page 100-101; 586pp; English.  
XX  
XX The present invention describes NOVX proteins, where X can be 1 to 55  
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide  
CC described above and a carrier; (2) a kit comprising, in one or more  
CC containers, the composition described above; (3) an isolated nucleic acid  
CC molecule which encodes a NOVX protein of the invention; (4) a vector  
CC comprising the nucleic acid molecule described above; (5) a cell  
CC comprising the above vector; (6) an antibody that immunospecifically  
CC binds to the polypeptide described above; (7) methods for determining the  
CC presence or amount of the above polypeptide or nucleic acid molecule in a  
CC sample; (8) methods for determining the presence of or predisposition to  
CC a disease associated with altered levels of expression of the above  
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a  
CC method of identifying an agent that binds to the polypeptide described  
CC above; (10) a method for identifying a potential therapeutic agent for  
CC use in treating a pathology that is related to an aberrant expression or  
CC aberrant physiological interactions of the polypeptide; (11) a method of  
CC screening for a modulator of activity or of latency or predisposition to  
CC a pathology associated with the polypeptide; (12) a method for modulating  
CC the activity of the polypeptide described above; (13) methods of treating  
CC or preventing a pathology associated with the above polypeptide in a  
CC mammal; and (14) a method for producing the above polypeptide. NOVX  
CC sequences have antidiabetic, anorectic, antibacterial, virucide,  
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian  
CC and antilipidemic activities, and can be used in gene therapy. The  
CC polypeptide is useful in manufacturing a medicament for treating a  
CC syndrome associated with a human disease. The polypeptide or the nucleic  
CC acid molecule may be used to diagnose, treat or prevent metabolic  
CC disorders such as diabetes or obesity, infections, cachexia, cancer,  
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's  
CC disease, immune disorders, haematopoietic disorders and various  
CC dyslipidaemias. The nucleic acids can also be used as hybridisation  
CC probes, in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. The present sequence represents a human NOVX from the  
XX present invention.  
SQ Sequence 623 AA;

Query Match 93.8%; Score 2440; DB 6; Length 623;  
Best Local Similarity 99.6%; Pred. No. 8.6e-238;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLFPE 60  
DB 5 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLFPE 64  
QY 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
DB 65 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 124  
QY 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYOPGG 180  
DB 125 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYOPGG 184  
QY 181 DLLSLNRYEDQDENLQYLAELILAVHSHVLMGVHRDIKPENILVDRTHGHIKLVDF 240  
DB 185 DLLSLNRYEDQDENLQYLAELILAVHSHVLMGVHRDIKPENILVDRTHGHIKLVDF 244  
QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDWMVSGVVIAYEMIYGR 300  
DB 245 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDWMVSGVVIAYEMIYGR 304  
QY 301 SPPAEGTSARTFNINMFORFLKPPDPKVSDFDLIQSLLCGQKRLKFEGLCCHPFF 360  
DB 305 SPPAEGTSARTFNINMFORFLKPPDPKVSDFDLIQSLLCGQKRLKFEGLCCHPFF 364

QY 361 SKIDWNINRNSPPFPVPTTLKSDDDTSNFDPEPKNSWSSPCQLSPSGSGBELPFGVGS 420  
DB 365 SKIDWNINRNSPPFPVPTTLKSDDDTSNFDPEPKNSWSSPCQLSPSGSGBELPFGVGS 424  
QY 421 YSKALGILGRSSESVVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKV 468  
DB 425 YSKALGILGRSSESVVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKM 472  
RESULT 10  
ID ABB81928  
XX ABB81928 standard; protein; 1958 AA.  
AC ABB81928;  
XX 10-OCT-2002 (first entry)  
DT Human kinase #2.  
DE Human kinase #2.  
XX Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;  
KW Citron rho-interacting kinase; gene therapy; mental disorder; cancer.  
XX Homo sapiens.  
OS WO200259325-A2.  
PN 01-AUG-2002.  
XX 20-DEC-2001; 2001WO-US050497.  
XX 27-DEC-2000; 2000US-0258335P.  
PR (LEXI-) LEXICON GENETICS INC.  
PA Yu X, Miranda M, Friddle CJ;  
PI WPI; 2002-599796/64.  
XX N-PSDB; ABQ78871.  
DR Novel polynucleotide encoding human proteins that are structurally  
XX similar to animal kinases, useful for drug screening, diagnosis, in gene  
PT therapy of disorders and diseases e.g. cancer and pharmacogenomic  
PT applications.  
XX Claim 4; Page 46-50; 50pp; English.  
PS The invention relates to a novel human protein that shares structural  
XX similarity with animal kinases, including serine-threonine kinases,  
CC particularly Citron rho-interacting kinases. The proteins of the  
CC invention have nootropic and cytostatic activity. The polynucleotides may  
CC have a use in gene therapy. The encoded novel polypeptides are useful for  
CC generating antibodies, as reagents in diagnostic assays, for identifying  
CC other cellular gene products related to NHP and as reagents in assays for  
CC screening for compounds that are useful in the treatment of mental,  
CC biological or medical disorders and diseases including cancer. The  
CC sequence represents a novel human kinase of the invention  
XX Sequence 1958 AA;  
SQ Query Match 93.8%; Score 2440; DB 5; Length 1958;  
Best Local Similarity 99.6%; Pred. No. 5.7e-237;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLFPE 60  
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLFPE 60  
QY 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
DB 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
QY 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYOPGG 180

Db 121 DIYAMKMKKALLAQEQVFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLYMEYQPGG 180  
QY 181 DLLSLNRYEDQDENLIOFYLAELILAVHSLMGVYVHRDIKPNILVDRTGHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIOFYLAELILAVHSLMGVYVHRDIKPNILVDRTGHIKLVDF 240  
QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDCDWSVGVIAYEMIYGR 300  
Db 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDCDWSVGVIAYEMIYGR 300  
QY 301 SPFAEGTSARTFNNIMNFORPLKFPDDPKVSSDFLDLIQSLLCQKERLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNNIMNFORPLKFPDDPKVSSDFLDLIQSLLCQKERLKFEGLCCHPFF 360  
QY 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468

RESULT 11

ABB81927  
ID ABB81927 standard; protein; 2054 AA.  
AC ABB81927;  
XX 10-OCT-2002 (first entry)  
XX Human kinase #1.  
XX Human; kinase; enzyme; serine-threonine kinase; neotropic; cytostatic;  
KW Citron rho-interacting kinase; gene therapy; mental disorder; cancer.  
XX Homo sapiens.  
XX WO200259325-A2.  
XX 01-AUG-2002.  
XX 20-DEC-2001; 2001WO-US050497.  
XX 27-DEC-2000; 2000US-0258335P.  
XX (LEXI-) LEXICON GENETICS INC.  
XX Yu X, Miranda M, Friddle C;  
PI WPI; 2002-599796/64.  
DR N-PSDB; ABQ78870.  
XX Novel polynucleotide encoding human proteins that are structurally  
PT similar to animal kinases, useful for drug screening, diagnosis, in gene  
PT therapy of disorders and diseases e.g. cancer and pharmacogenomic  
PT applications.  
XX Claim 2; Page 39-43; 50pp; English.

XX The invention relates to a novel human protein that shares structural  
CC similarity with animal kinases, including serine-threonine kinases,  
CC particularly Citron rho-interacting kinases. The proteins of the  
CC invention have neotropic and cytostatic activity. The polynucleotides may  
CC have a use in gene therapy. The encoded novel polypeptides are useful for  
CC generating antibodies, as reagents in diagnostic assays, for identifying  
CC other cellular gene products related to NHP and as reagents in assays for  
CC screening for compounds that are useful in the treatment of mental,  
CC biological or medical disorders and diseases including cancer. The  
CC sequence represents a novel human kinase of the invention  
XX Sequence 2054 AA;

Query Match 93.8%; Score 2440; DB 5; Length 2054;  
Best Local Similarity 99.8%; Pred. No. 6.1e-237;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPFPMTQQQMSPLSRREGILDALFVLF 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPFPMTQQQMSPLSRREGILDALFVLF 60  
QY 61 ECQPALMKIKHVSNTFRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
Db 61 ECQPALMKIKHVSNTFRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
QY 121 DIYAMKMKKALLAQEQVFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLYMEYQPGG 180  
Db 121 DIYAMKMKKALLAQEQVFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLYMEYQPGG 180  
QY 181 DLLSLNRYEDQDENLIOFYLAELILAVHSLMGVYVHRDIKPNILVDRTGHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIOFYLAELILAVHSLMGVYVHRDIKPNILVDRTGHIKLVDF 240  
QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDCDWSVGVIAYEMIYGR 300  
Db 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDCDWSVGVIAYEMIYGR 300  
QY 301 SPFAEGTSARTFNNIMNFORPLKFPDDPKVSSDFLDLIQSLLCQKERLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNNIMNFORPLKFPDDPKVSSDFLDLIQSLLCQKERLKFEGLCCHPFF 360  
QY 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468

RESULT 12  
AAE24150  
ID AAE24150 standard; protein; 2054 AA.  
XX AAE24150;  
XX 23-SEP-2002 (first entry)  
XX Human kinase (PKIN)-21 protein.  
XX Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;  
KW acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;  
KW asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;  
KW development; hepatitis; cardiovascular; hypertension; drug screening;  
KW myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;  
KW fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;  
KW hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hiv;  
KW neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;  
XX hyperlipidaemia; enzyme.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Domain 97.360  
FT /note="Eukaryotic protein kinase domain"  
FT Domain 98.241  
FT /note="Protein kinase domain"  
FT Domain 99.349  
FT /note="Protein kinase domain"  
FT Domain 101.241  
FT /note="Protein kinase domain"  
FT Domain 102.241  
FT /note="Protein kinase domain"  
FT Domain 249.349  
FT /note="Protein kinase domain"  
FT Domain 258.445



CC associated with the polypeptide dysfunction. The expression vector or the  
 CC reagent is useful in the preparation of a medicament for modulating the  
 CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
 CC disease, such as obesity or chronic obstructive pulmonary disease. These  
 CC may also be used for treating obesity/ overweight-associated  
 CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
 CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
 CC apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced  
 CC fertility, and depression  
 XX  
 SQ Sequence 495 AA;

Query Match 99.2%; Score 2582; DB 6; Length 495;  
 Best Local Similarity 99.8%; Pred. No. 2.3e-252;  
 Matches 494; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGNPLDAGAEPTANPASRLNLFQCKPPTMTQQMSPLREGILDALFVLE 60  
 DB 1 MLKFKYGNPLDAGAEPTANPASRLNLFQCKPPTMTQQMSPLREGILDALFVLE 60  
 QY 61 ECSQPALMKIKHVSFNFRKYSYDTIAELQELQPSAKDPEVRSVLCGCHFAEVQVVRKATG 120  
 DB 61 ECSQPALMKIKHVSFNFRKYSYDTIAELQELQPSAKDPEVRSVLCGCHFAEVQVVRKATG 120  
 QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180  
 DB 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPGG 180  
 QY 181 DLLSLNRYEDQDENLIQYLAELILAVSHVLMGVVHRDIKPENILVDRTHGKLVDF 240  
 DB 181 DLLSLNRYEDQDENLIQYLAELILAVSHVLMGVVHRDIKPENILVDRTHGKLVDF 240  
 QY 241 GSAAKWNSNKNVNAKPIGTPDYMAPEVLTVMNGDGKGTGVLCDWMSVGVIAEYMIYGR 300  
 DB 241 GSAAKWNSNKNVNAKPIGTPDYMAPEVLTVMNGDGKGTGVLCDWMSVGVIAEYMIYGR 300  
 QY 301 SPFAEGTSARTFNINMFRFLKFPDDPKVSSDFLDLIQSLLCGKERLKFEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNINMFRFLKFPDDPKVSSDFLDLIQSLLCGKERLKFEGLCCHPFF 360  
 QY 361 SKIDWNNIRNSPPFPVPTLKSDDDTNFDPEKNWSVSSPCQLSPSGSGEELPFVFGFS 420  
 DB 361 SKIDWNNIRNSPPFPVPTLKSDDDTNFDPEKNWSVSSPCQLSPSGSGEELPFVFGFS 420  
 QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFTSAAGLLPCSR 480  
 DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFTSAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGC 495  
 DB 481 ILPSVYAKSGARGC 495

RESULT 8  
 ID ADN62809  
 XX ADN62809 standard; protein; 620 AA.  
 XX  
 AC ADN62809;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human NOV1b.  
 XX  
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;  
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; immune disorder;  
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;  
 KW wasting disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004038223-A1.  
 XX

PD 26-FEB-2004.  
 XX 01-OCT-2002; 2002US-00262511.  
 XX 02-OCT-2001; 2001US-0326483P.  
 PR 05-OCT-2001; 2001US-0327435P.  
 PR 05-OCT-2001; 2001US-0327449P.  
 PR 09-OCT-2001; 2001US-0327917P.  
 PR 09-OCT-2001; 2001US-0328029P.  
 PR 09-OCT-2001; 2001US-0328044P.  
 PR 09-OCT-2001; 2001US-0328056P.  
 PR 12-OCT-2001; 2001US-0328849P.  
 PR 15-OCT-2001; 2001US-0329414P.  
 PR 17-OCT-2001; 2001US-0330142P.  
 PR 18-OCT-2001; 2001US-0330309P.  
 PR 22-OCT-2001; 2001US-0341058P.  
 PR 24-OCT-2001; 2001US-0342666P.  
 PR 24-OCT-2001; 2001US-0343629P.  
 PR 29-OCT-2001; 2001US-0349575P.  
 PR 01-NOV-2001; 2001US-0346357P.  
 PR 17-APR-2002; 2002US-0373260P.  
 PR 19-APR-2002; 2002US-0373815P.  
 PR 19-APR-2002; 2002US-0373817P.  
 PR 19-APR-2002; 2002US-0373826P.  
 PR 19-APR-2002; 2002US-0373884P.  
 PR 22-APR-2002; 2002US-0374977P.  
 PR 16-MAY-2002; 2002US-0381037P.  
 PR 16-MAY-2002; 2002US-0381038P.  
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 PR 17-MAY-2002; 2002US-0381642P.  
 PR 28-MAY-2002; 2002US-0383656P.  
 PR 29-MAY-2002; 2002US-0383831P.  
 XX 25-JUN-2002; 2002US-0391335P.  
 XX (SMIT/) SMITHSON G.  
 PA (MILL/) MILLET I.  
 PA (PEYM/) PEYMAN J A.  
 PA (KEKU/) KEKUDA R.  
 PA (JUJG/) JU J.  
 PA (LILL/) LI L.  
 PA (GUOX/) GUO X.  
 PA (PATT/) PATTURAJAN M.  
 PA (SPY2/) SPYTEK K A.  
 PA (EDIN/) EDINGER S R.  
 PA (ELLE/) ELLERMAN K.  
 PA (MALY/) MALYANKAR U M.  
 PA (ORTT/) ORT T.  
 PA (GORM/) GORMAN L.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (ANDE/) ANDERSON D W.  
 PA (ZHON/) ZHONG M.  
 PA (CATT/) CATTERTON E.  
 PA (JIWW/) JI W.  
 PA (MILL/) MILLER C E.  
 PA (RAST/) RASTELLI L.  
 PA (STON/) STONE D J.  
 PA (PENA/) PENNA C E A.  
 PA (SHEN/) SHENOY S G.  
 PA (SHIM/) SHIMKETS R A.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (LEAC/) LEACH M D.  
 PA (AGEE/) AGE E M L.  
 PA (BERG/) BERGHS C.  
 PA (DIPI/) DIPIPO V A.  
 PA (EISE/) EISEN A.  
 PA (GANG/) GANGOLLI E A.  
 PA (RIEG/) RIEGER D K.  
 PA (SPAD/) SPADERNA S K.  
 XX  
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;  
 PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;  
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;  
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;

PI Shimkets RA, Rotherberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;  
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;  
XX WPI; 2004-213931/20.  
DR N-PSDB; ADN62808.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,  
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.  
XX Claim 1; SEQ ID NO 4; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.  
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or  
CC treat a medical condition in human related to the aberrant expression and  
CC activity of NOVX polypeptides. For example, NOVX polypeptides and  
CC polynucleotides may be used to treat disorders associated with decreased  
CC expression or activity of NOVX by supplementing the patient our  
CC production or to rectify mutations. Conversely, antisense NA molecules  
CC may be administered to down regulate expression of NOVX polypeptides by  
CC binding with the cells own genes and preventing their expression. NOVX  
CC polynucleotides and complementary sequences may also be used as DNA  
CC probes in diagnostic assays to detect and quantitate the presence of  
CC similar sequences in samples, and so which patients may be in need of  
CC restorative therapy. NOVX polypeptides may also be used as antigens in  
CC the production of antibodies and in assays to identify modulators  
CC (agonists and antagonists) of the expression and activity of NOVX. The  
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be  
CC used to modulate NOVX polynucleotide expression and activity of NOVX  
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as  
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX  
CC polypeptides and polynucleotides may be used in this way to prevent,  
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious  
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative  
CC disorders, Alzheimer's Disease, Parkinson's disorder, immune disorders,  
CC haematopoietic disorders, and the various dyslipidaemias, metabolic  
CC disturbances associated with obesity, the metabolic syndrome X and  
CC wasting disorders associated with chronic diseases and various cancers.  
CC They may also be used as antibacterial agents. The present sequence  
CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 620 AA;

Query Match 93.8%; Score 2440; DB 8; Length 620;  
Best Local Similarity 99.6%; Pred. No. 8.5e-238;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARPLDGAARPTANRASRLNLFQKPPMTQQQMSPLSREGILDALFVLF 60  
DB 5 MLKFKYGARPLDGAARPTANRASRLNLFQKPPMTQQQMSPLSREGILDALFVLF 64  
QY 61 ECSQPALMKTKHVSNFVRKYSDTIAELQELQPSAKDFEVSILGCGHFAEVQVREKATG 120  
DB 65 ECSQPALMKTKHVSNFVRKYSDTIAELQELQPSAKDFEVSILGCGHFAEVQVREKATG 124  
QY 121 DIYAMVKMKKALLAQOVQSFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVYQPGG 180  
DB 125 DIYAMVKMKKALLAQOVQSFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMVYQPGG 184  
QY 181 DLLSLNRYEDOLDENLIQVLAELILAVHSHVLMGVYHVDIKPENILVDRTHIKLVDF 240  
DB 185 DLLSLNRYEDOLDENLIQVLAELILAVHSHVLMGVYHVDIKPENILVDRTHIKLVDF 244  
QY 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMGDGGTYGLDCDWMVSGVIAYEIMYGR 300  
DB 245 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMGDGGTYGLDCDWMVSGVIAYEIMYGR 304  
QY 301 SPFAEGTSARTFNIMNFRLKFPDDPKVSSPDLIIQSLCCQKRLKFEGLCCHPFF 360  
DB 305 SPFAEGTSARTFNIMNFRLKFPDDPKVSSPDLIIQSLCCQKRLKFEGLCCHPFF 364  
QY 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSSPCOLSPGFSGEELPFVGF 420  
DB 365 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSSPCOLSPGFSGEELPFVGF 424

QY 421 YSKALGILGRSESVVGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
DB 425 YSKALGILGRSESVVGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 472

RESULT 9  
ADA05644

ID ADA05644 standard; protein; 623 AA.

XX AC ADA05644;

XX DT 06-NOV-2003 (first entry)

XX DE Human NOV1b protein SEQ ID NO:4.

XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;  
KW immunomodulator; cytostatic; nootropic; neuroprotective;  
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;  
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;  
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX OS Homo sapiens.

XX WC2003029424-A2.

XX PD 10-APR-2003.

XX PF 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 05-OCT-2001; 2001US-0327449P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 09-OCT-2001; 2001US-0328056P.

XX PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330309P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 24-OCT-2001; 2001US-0343629P.

XX PR 29-OCT-2001; 2001US-0349575P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 19-APR-2002; 2002US-0373884P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 17-MAY-2002; 2002US-0381042P.

XX PR 28-MAY-2002; 2002US-0383656P.

XX PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391335P.

XX PR 01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

XX Smithson G, Millett I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;  
XX Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;  
XX Ort T, Gorman L, Zerkhus BD, Anderson DW, Zhong M, Catterton E;  
XX Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shency SG;  
XX Shimkets RA, Rotherberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;  
XX Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2003-381626/36.

XX N-PSDB; ADA05643.

181 DLLSLNRYEDQDENLQFYLAELILAVHSHLMGVVHRDIKPENILVDRTGHIKLVDF 240  
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181 DLLSLNRYEDQDENLQFYLAELILAVHSHLMGVVHRDIKPENILVDRTGHIKLVDF 240  
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Db 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVMGDGKGTGLDCDMSVGVIAEMLYGR 300  
Qy 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLSLCGQKXERLKFEGLCCHPFF 360  
Db 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLSLCGQKXERLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
Qy 421 YKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELODQSKCHKVFI SAAGLLPCSR 480  
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RESULT 2  
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; Sequence 2, Application US/10238709  
; Publication No. US20030022340A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-10-724-709-2

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Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYOPGG 180  
Db 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYOPGG 180  
Qy 181 DLLSLNRYEDQDENLQFYLAELILAVHSHLMGVVHRDIKPENILVDRTGHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLQFYLAELILAVHSHLMGVVHRDIKPENILVDRTGHIKLVDF 240  
Qy 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVMGDGKGTGLDCDMSVGVIAEMLYGR 300  
Db 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVMGDGKGTGLDCDMSVGVIAEMLYGR 300  
Qy 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLSLCGQKXERLKFEGLCCHPFF 360  
Db 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLSLCGQKXERLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
Qy 421 YKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELODQSKCHKVFI SAAGLLPCSR 480  
Db 421 YKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELODQSKCHKVFI SAAGLLPCSR 480  
Qy 481 ILPSVYAKGSARGRCWL 497  
Db 481 ILPSVYAKGSARGRCWL 497

361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
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Qy 421 YKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELODQSKCHKVFI SAAGLLPCSR 480  
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Qy 481 ILPSVYAKGSARGRCWL 497  
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; Sequence 2, Application US/10724594  
; Publication No. US20040091993A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164DIV II  
; CURRENT APPLICATION NUMBER: US/10/724,594  
; CURRENT FILING DATE: 2003-12-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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Db 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYOPGG 180  
Qy 181 DLLSLNRYEDQDENLQFYLAELILAVHSHLMGVVHRDIKPENILVDRTGHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLQFYLAELILAVHSHLMGVVHRDIKPENILVDRTGHIKLVDF 240  
Qy 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVMGDGKGTGLDCDMSVGVIAEMLYGR 300  
Db 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVMGDGKGTGLDCDMSVGVIAEMLYGR 300  
Qy 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLSLCGQKXERLKFEGLCCHPFF 360  
Db 301 SPPAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLIQLSLCGQKXERLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
Qy 421 YKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELODQSKCHKVFI SAAGLLPCSR 480  
Db 421 YKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELODQSKCHKVFI SAAGLLPCSR 480  
Qy 481 ILPSVYAKGSARGRCWL 497  
Db 481 ILPSVYAKGSARGRCWL 497

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:40:07 ; Search time 146 Seconds  
(without alignments)  
1125.198 Million cell updates/sec

Title: US-10-724-594-2

Perfect score: 2602

Sequence: 1 MLKFYKARNPLDAGAAEPI.....CSRILPSVYAKSGARGCWL 497

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1401741 seqs, 330541175 residues

Total number of hits satisfying chosen parameters: 1401741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2602	100.0	497	9	US-09-804-471A-2
2	2602	100.0	497	14	US-10-238-709-2
3	2602	100.0	497	15	US-10-724-594-2
4	2589	99.5	497	15	US-10-311-034-7
5	2440	93.8	623	13	US-10-262-511-4
6	2440	93.8	1958	13	US-10-028-946-4
7	2440	93.8	2054	13	US-10-028-946-2
8	2440	93.8	2054	13	US-10-415-011-21
9	2430	93.4	2053	13	US-10-017-216-2
10	2430	93.4	2053	13	US-10-325-430-12
11	2430	93.4	2053	16	US-10-757-262-52
12	2418.5	92.9	2055	16	US-10-618-941-67
13	2412.5	92.7	2053	11	US-09-964-956-11

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15	2412.5	92.7	2066	11	US-09-964-956-9	Sequence 9, Appli
16	2412.5	92.7	2066	15	US-10-262-511-14	Sequence 14, Appli
17	2271.5	87.3	494	9	US-09-804-471A-4	Sequence 4, Appli
18	2271.5	87.3	494	14	US-10-238-709-4	Sequence 4, Appli
19	2271.5	87.3	494	15	US-10-724-594-4	Sequence 4, Appli
20	2172.5	83.5	2055	13	US-10-017-216-4	Sequence 4, Appli
21	1652	63.5	319	15	US-10-412-897-2	Sequence 2, Appli
22	1284	49.3	257	14	US-10-282-048-2	Sequence 2, Appli
23	1180	45.3	251	14	US-10-282-048-4	Sequence 4, Appli
24	1177	45.2	251	14	US-10-282-048-5	Sequence 5, Appli
25	1177	45.2	251	14	US-10-282-048-6	Sequence 6, Appli
26	932.5	35.8	1565	16	US-10-702-496-2	Sequence 2, Appli
27	929	35.7	475	15	US-10-415-011-2	Sequence 2, Appli
28	929	35.7	1572	15	US-10-333-314-20	Sequence 20, Appli
29	929	35.7	1572	16	US-10-618-941-68	Sequence 68, Appli
30	908.5	34.9	1548	15	US-10-369-493-6347	Sequence 6347, Ap
31	896.5	34.5	1000	15	US-10-012-697-1540	Sequence 1540, Ap
32	896.5	34.5	1711	9	US-09-771-161A-219	Sequence 219, App
33	896.5	34.5	1711	9	US-09-771-161A-220	Sequence 220, App
34	896.5	34.5	1711	15	US-10-399-225-10	Sequence 10, Appl
35	896.5	34.5	1711	17	US-10-781-581-206	Sequence 206, App
36	896.5	34.5	1711	17	US-10-753-267-72	Sequence 72, Appl
37	891	34.2	496	9	US-09-771-161A-228	Sequence 228, App
38	891	34.2	1719	15	US-10-288-798-2	Sequence 2, Appli
39	891	34.2	1719	15	US-10-362-892-2	Sequence 2, Appli
40	891	34.2	1770	15	US-10-433-794-19	Sequence 19, Appl
41	890	34.2	1572	16	US-10-702-496-4	Sequence 4, Appli
42	882.5	33.9	1664	15	US-10-210-130-102	Sequence 102, App
43	882.5	33.9	1738	15	US-10-210-130-100	Sequence 100, App
44	877.5	33.7	573	9	US-09-764-868-671	Sequence 671, App
45	877.5	33.7	573	11	US-09-764-875-1205	Sequence 1205, Ap

ALIGNMENTS

RESULT 1

US-09-804-471A-2  
; Sequence 2, Application US/09804471A  
; Patent No. US20020132322A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: C0001164  
; CURRENT APPLICATION NUMBER: US/09/804,471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-09-804-471A-2

Query Match 100.0%; Score 2602; DB 9; Length 497;  
Best Local Similarity 100.0%; Pred. No. 4.9e-190;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLKFYKARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSRGILDALFVLF	60
Db	1	MLKFYKARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSRGILDALFVLF	60
Qy	61	ECSPALMKIKHVSFNVRKYSYDTIAELQPSAKDFEVRSLVGCGHFAEVQVVRKATG	120
Db	61	ECSPALMKIKHVSFNVRKYSYDTIAELQPSAKDFEVRSLVGCGHFAEVQVVRKATG	120
Qy	121	DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPQYAFQDKNHLVLMYEQPG	180
Db	121	DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPQYAFQDKNHLVLMYEQPG	180

FT Domain /note= "Protein kinase domain"  
 FT 258. .349  
 FT /note= "Protein kinase domain"  
 FT 534. .542  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 854. .875  
 FT /note= "Leucine zipper pattern"  
 FT 891. .933  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 964. .975  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 991. .1012  
 FT /note= "Leucine zipper pattern"  
 FT 1015. .1067  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1057. .1078  
 FT /note= "Leucine zipper pattern"  
 FT 1159. .1180  
 FT /note= "Leucine zipper pattern"  
 FT 1217. .1255  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1388. .1434  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1390. .1438  
 FT /note= "Phorbol esters/diacylglycerol binding site"  
 FT 1403. .1466  
 FT /note= "Phorbol esters/diacylglycerol binding site"  
 FT 1471. .1590  
 FT /note= "PH domain"  
 FT 1619. .1916  
 FT /note= "CNH domain"  
 FT 1759. .1802  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1819. .1831  
 FT /note= "Domain found in NIK1-like kinase"  
 FT 1851. .1880  
 FT /note= "Domain found in NIK1-like kinase"  
 FT  
 XX W020233099-A2.  
 XX  
 XX 25-APR-2002.  
 XX  
 XX 20-OCT-2001; 2001WO-US047728.  
 XX  
 XX 20-OCT-2000; 2000US-0242410P.  
 PR 27-OCT-2000; 2000US-0244068P.  
 PR 03-NOV-2000; 2000US-0245708P.  
 PR 09-NOV-2000; 2000US-0247672P.  
 PR 16-NOV-2000; 2000US-0249565P.  
 PR 22-NOV-2000; 2000US-0252730P.  
 PR 01-DEC-2000; 2000US-0250807P.  
 XX  
 XX (INCYTE) INCYTE GENOMICS INC.  
 XX  
 PI Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C;  
 PI Yao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;  
 PI Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;  
 PI Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;  
 PI Thangavelu K, Khan FA, Ison CH;  
 XX  
 XX WPI; 2002-454603/48.  
 DR N-PSDB; AAD38864.  
 DR  
 XX New human kinase polypeptide, for diagnosing, preventing and treating  
 PT cancer, immune system disorders, growth and development disorders,  
 PT cardiovascular disorders and lipid disorders.  
 XX  
 XX Claim 1; Page 177-182; 210pp; English.  
 XX  
 CC The invention relates human kinases (PKIN) and their corresponding  
 CC nucleic acid sequences. PKIN and its DNA are useful for diagnosing,  
 CC treating and preventing cancer, an immune system disorder (e.g., acquired  
 CC immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,

CC atherosclerosis, multiple sclerosis, psoriasis), disorders affecting  
 CC growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),  
 CC cardiovascular disorder (e.g., hypertension, myocardial infarction,  
 CC Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,  
 CC Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,  
 CC hyperlipidaemia, obesity), and for assessing the effects of exogenous  
 CC compounds. Anti-PKIN antibody is useful in a diagnostic test for a  
 CC condition or a disease associated with the expression of PKIN in a  
 CC biological sample. A composition comprising PKIN or an agonist or  
 CC antagonist of PKIN is useful for treating a disease or condition  
 CC associated with decreased or increased expression of functional PKIN.  
 CC PKIN is useful in a number of drug screening techniques and to analyse  
 CC the proteome of a tissue or cell type. PKIN DNA is useful for creating  
 CC knockin humanised animals or transgenic animals to model human diseases,  
 CC and in somatic or germline gene therapy. The present sequence is human  
 CC PKIN protein  
 XX  
 SQ Sequence 2054 AA;  
 Query Match 93.8%; Score 2440; DB 5; Length 2054;  
 Best Local Similarity 99.6%; Pred. No. 6.1e-237;  
 Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLKFKYGARNPLDAGAAEPIANRSLNLFQCKPFPMTQQQMSPLSRREGILDALFVLFE 60  
 DB 1 MLKFKYGARNPLDAGAAEPIASRLNLFQCKPFPMTQQQMSPLSRREGILDALFVLFE 60  
 QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGGHFAVQVVRKATG 120  
 DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGGHFAVQVVRKATG 120  
 QY 121 DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPGG 180  
 DB 121 DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPGG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHMGVYHRDIKPENILVDRTGHIKLVDF 240  
 DB 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHMGVYHRDIKPENILVDRTGHIKLVDF 240  
 QY 241 GSAAKNSNMKNVNAKLPIGTPTMAPEVLTVNMGDKGTGYGLDCDWMSVGVIAEYMYGR 300  
 DB 241 GSAAKNSNMKNVNAKLPIGTPTMAPEVLTVNMGDKGTGYGLDCDWMSVGVIAEYMYGR 300  
 QY 301 SPFAEGTSARTFNNIMNFQFLKFPDDPKVSSDFLDLIQSLLCGQKRLKPEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNNIMNFQFLKFPDDPKVSSDFLDLIQSLLCGQKRLKPEGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSPCQLSPGSGEELPFVGFSS 420  
 DB 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSPCQLSPGSGEELPFVGFSS 420  
 QY 421 YSKALGILGRSESVWSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 DB 421 YSKALGILGRSESVWSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 RESULT 13  
 AAO26959  
 ID AAO26959 standard; protein; 2054 AA.  
 XX  
 AC AAO26959;  
 XX  
 DT 01-MAY-2003 (first entry)  
 XX  
 DE Human CRUK protein sequence, SEQ ID No 2.  
 KW Aorectic; hypotensive; cardiant; antilipaeamic; cerebroprotective;  
 KW antigout; osteopathic; antiarthritic; cytostatic; antidepressant;  
 KW immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;  
 KW neuroprotective; antiinflammatory; antidiabetic; analgesic;  
 KW human citron rho/rac-interacting kinase; enzyme; CRUK; ameliorating;  
 KW obesity; comorbidities; cancer; anorexia; cachexia; bulimia;  
 KW central nervous system disorder; chronic obstructive pulmonary disease;



CC (MDPK) polypeptides designated as 13245 and nucleic acid molecules  
CC encoding such polypeptides. 13245 molecules are used to develop  
CC diagnostic and therapeutic agents for prognosticating, diagnosing,  
CC preventing, inhibiting, alleviating or curing MDPK-related disorders.  
CC Polypeptides of the invention are used to develop diagnostic and  
CC therapeutic agents for 13245-mediated or related disorders such as  
CC tumorigenesis, tumour growth, tumour metastasis, viral infection of a  
CC cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies),  
CC immune disorders and neoplastic disorders. The invention is also used in  
CC gene therapy. The present sequence is human MDPK protein  
XX  
SQ Sequence 2053 AA;

Query Match 93.4%; Score 2430; DB 5; Length 2053;  
Best Local Similarity 99.1%; Pred. No. 6.3e-236;  
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
QY 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
DB 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180  
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180  
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240  
QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAIYEMIYGR 300  
DB 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAIYEMIYGR 300  
QY 301 SPPAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIOQLLQCGKERLKFEGLCCHPFF 360  
DB 301 SPPAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIOQLLQCGKERLKFEGLCCHPFF 360  
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

RESULT 15  
ADP60994  
ID ADP60994 standard; protein; 2053 AA.  
XX  
AC ADP60994;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Pain associated human 2207 polypeptide.  
XX  
KW Pain modulation; pain disorder; painful disorder; potassium channel;  
KW kinase expression; inflammatory pain; chronic pain; neuropathic pain;  
KW causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain;  
KW analgesic; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
PN US2003153525-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 19-DEC-2002; 2002US-00325430.  
XX

PR 19-DEC-2001; 2001US-0341953P.  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX  
XX Silos-Santiago I, Rosenfeld JB;  
XX  
XX WPI; 2003-897732/82.  
DR N-PSDB; ADF60992, ADF60993.  
XX  
XX Identifying a compound capable of treating a pain disorder comprises  
XX assaying the ability of the compound to modulate specific, e.g., kinases  
XX or potassium channel, nucleic acid expression or polypeptide activities.  
XX  
XX Disclosure; SEQ ID NO 12; 80pp; English.  
PS  
XX The present invention relates to a method for identifying a compound  
XX capable of modulating pain or painful disorders. The method comprises  
XX assaying the ability of the compound to modulate specific nucleic acid  
XX expression or polypeptide activity e.g. potassium channel, or kinase  
XX expression/activity. The method and compounds are useful for treating  
XX pain or painful disorders e.g. inflammatory pain, chronic pain,  
XX neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache  
XX pain and tissue pain. The present sequence represents a human protein  
XX associated with pain.  
XX  
SQ Sequence 2053 AA;

Query Match 93.4%; Score 2430; DB 7; Length 2053;  
Best Local Similarity 99.1%; Pred. No. 6.3e-236;  
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPFMTQQQMSPLSREGILDALFVLF 60  
QY 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
DB 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG 120  
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180  
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLYMEYQPG 180  
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240  
QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAIYEMIYGR 300  
DB 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAIYEMIYGR 300  
QY 301 SPPAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIOQLLQCGKERLKFEGLCCHPFF 360  
DB 301 SPPAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIOQLLQCGKERLKFEGLCCHPFF 360  
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468

Search completed: March 18, 2005, 15:37:01  
Job time : 179 secs





Result No.	Query			DB	ID	Description
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1	945.4	63.8	957	1	PCT-US03-11189-1	Sequence 1, Appli
2	925	62.5	1048	7	US-10-450-763-15557	Sequence 15557, A
3	225.6	15.2	1830	7	US-10-450-763-23273	Sequence 23273, A
4	225.6	15.2	6303	7	US-10-450-763-21232	Sequence 21332, A
5	213.2	14.4	5754	7	US-10-450-763-13871	Sequence 13871, A
6	202.4	13.7	204	1	PCT-US03-11189-11	Sequence 11, Appli
7	196	13.2	5333	1	PCT-US04-42360-13	Sequence 13, Appli
8	176	11.9	176	1	PCT-US03-11189-7	Sequence 7, Appli
9	175.6	11.9	4055	7	US-10-450-763-17152	Sequence 17152, A
10	171.8	11.6	489	8	US-11-060-756-1334	Sequence 1334, Ap
11	171.8	11.6	489	8	US-11-060-756-1335	Sequence 1335, Ap
12	171.8	11.6	489	8	US-11-060-756-5606	Sequence 5606, Ap
13	171.8	11.6	489	8	US-11-060-756-5607	Sequence 5607, Ap
14	143	9.7	143	1	PCT-US03-11189-9	Sequence 9, Appli
15	142	9.6	142	1	PCT-US03-11189-6	Sequence 6, Appli
16	131	8.2	3393	1	PCT-US04-42360-673	Sequence 673, App
17	106.8	7.2	2304	6	US-10-932-182A-2150	Sequence 2150, Ap
18	102	6.9	102	1	PCT-US03-11189-8	Sequence 8, Appli
19	98.4	6.6	1695	6	US-10-932-182A-3703	Sequence 2703, Ap
20	97.4	6.6	1695	6	US-10-932-182A-79012	Sequence 79012, A
21	96.2	6.5	1572	6	US-10-932-182A-81056	Sequence 81056, A
22	94	6.3	94	1	PCT-US03-11189-10	Sequence 10, Appli
23	92.2	6.2	1951	1	PCT-US03-35712-114	Sequence 114, App
24	92.2	6.2	2945	1	PCT-US03-35712-115	Sequence 115, App

301 GTTGTGCTCACTTGTCTGAAGTGCAGGTGCTTAAGAGAGAAAGCAACCGGGACATCTATG 360  
Db |||||  
311 GTTGTGCTCACTTGTCTGAAGTGCAGGTGCTTAAGAGAGAAAGCAACCGGGACATCTATG 370  
Qy |||||  
361 CTATGAAGTGTATGAAGAAGGCTTTATTTGGCCCGAGGAGGTTTCAATTTTGGAG 420  
Db |||||  
371 CTATGAAGTGTATGAAGAAGGCTTTATTTGGCCCGAGGAGGTTTCAATTTTGGAG 430  
Qy |||||  
421 AAGAGCGGACATATTTCTCGAAGCAACCGCGTGGATCCCCCAATTAAGATGCTT 480  
Db |||||  
431 AAGAGCGGACATATTTCTCGAAGCAACCGCGTGGATCCCCCAATTAAGATGCTT 490  
Qy |||||  
481 TTCAAGCAAAATACACCTTTATCTGCTCATGGAATATCAGCTTGGAGGGGACTTGTGT 540  
Db |||||  
491 TTCAAGCAAAATACACCTTTATCTGCTCATGGAATATCAGCTTGGAGGGGACTTGTGT 550  
Qy |||||  
541 CACTTTTGAATAGATATGAGGACCGATTAGATGAAAACCTTGATACAGTTTACCTAGCTG 600  
Db |||||  
551 CACTTTTGAATAGATATGAGGACCGATTAGATGAAAACCTTGATACAGTTTACCTAGCTG 610  
Qy |||||  
601 AGCTGATTTGGCTGTTTCAGAGGTTTCATCTGATGGATACGTGTCATCGAGATCAAGC 660  
Db |||||  
611 AGCTGATTTGGCTGTTTCAGAGGTTTCATCTGATGGATACGTGTCATCGAGATCAAGC 670  
Qy |||||  
661 CTGAGAACATTTCTGTTGACCGCACAGACACATCAAGCTGTTGGATTTGGGATCTGCCG 720  
Db |||||  
671 CTGAGAACATTTCTGTTGACCGCACAGACACATCAAGCTGTTGGATTTGGGATCTGCCG 730  
Qy |||||  
721 CGAAATGAATTCAAACAGATGGTGAATCCAAATCCCGATTTGGGACCCAGATTACA 780  
Db |||||  
731 CGAAATGAATTCAAACAGATGGTGAATCCAAATCCCGATTTGGGACCCAGATTACA 790  
Qy |||||  
781 TGCTCTCGAAGTCTGACTGATGACCGGATGGAAGGACCTACGGCTGGACT 840  
Db |||||  
791 TGCTCTCGAAGTCTGACTGATGACCGGATGGAAGGACCTACGGCTGGACT 850  
Qy |||||  
841 GTCACTGCTGCTCAGTGGGCTGATTCCTATGAGATGATTTATGGAGATCCCCCTTCG 900  
Db |||||  
851 GTCACTGCTGCTCAGTGGGCTGATTCCTATGAGATGATTTATGGAGATCCCCCTTCG 910  
Qy |||||  
901 CAGAGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAG 947  
Db |||||  
911 CAGAGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAG 957

RESULT 2  
US-10-450-763-15557  
; Sequence 15557, Application US/10450763  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 15557  
; LENGTH: 1048  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (412)..(909)  
; OTHER INFORMATION: 77% homologous to Mus musculus Pro-Pol-dutPase  
; OTHER INFORMATION: polypeptide, accession number Y12713, Smith-Waterman Score=685.  
US-10-450-763-15557

Query Match 62.5%; Score 925; DB 7; Length 1048;  
Best Local Similarity 99.5%; Pred. No. 3.7e-235;  
Matches 928; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 15 CGGAATCCCTTTTGGATGCTGCTGAACCCATTTGCCAACCGGGCTTCAGGCTGAAT 74  
Db |||||  
116 CGGAATCCCTTTTGGATGCTGCTGAACCCATTTGCCAACCGGGCTTCAGGCTGAAT 175  
Qy 75 CTGTTCTTCAGGGGAAACACCCCTTTATGACTCAACAGAGATGCTCTCTTTCCGA 134  
Db |||||  
176 CTGTTCTTCAGGGGAAACACCCCTTTATGACTCAACAGAGATGCTCTCTTTCCGA 235  
Qy 135 GAAGGATATTTAGATCCCTCTTTGTTCTCTTTTGAAGAATGCACTGCTGCTGATG 194  
Db |||||  
236 GAAGGATATTTAGATCCCTCTTTGTTCTCTTTTGAAGAATGCACTGCTGCTGATG 295  
Qy 195 AAGATTAAAGCAGCTGAGCAACTTTTGTCCGGAAGTATTTCCGACACCATAGCTGATTA 254  
Db |||||  
296 AAGATTAAAGCAGCTGAGCAACTTTTGTCCGGAAGTATTTCCGACACCATAGCTGATTA 355  
Qy 255 GAGCTCCAGCTTCGGCAAGGACTTCGAAAGTCAGAAAGTCTTGTAGTGTGTGCTCACTTT 314  
Db |||||  
356 GAGCTCCAGCTTCGGCAAGGACTTCGAAAGTCAGAAAGTCTTGTAGTGTGTGCTCACTTT 415  
Qy 315 GCTGAAGTGCAGGTGCTTAAGAGAAAGCAACCGGGGACATCTATGCTATGAAGTATG 374  
Db |||||  
416 GCTGAAGTGCAGGTGCTTAAGAGAAAGCAACCGGGGACATCTATGCTATGAAGTATG 475  
Qy 375 AAGAAGAGGCTTTATTTGGCCCGAGGAGGTTTCAATTTTGGAGGAGCGGAAACATA 434  
Db |||||  
476 AAGAAGAGGCTTTATTTGGCCCGAGGAGGTTTCAATTTTGGAGGAGCGGAAACATA 535  
Qy 435 TTATCTCGAAGCAACAGCCCGTGGATCCCCCAATTAAGATGCTCTTCAGGACAAAT 494  
Db |||||  
536 TTATCTCGAAGCAACAGCCCGTGGATCCCCCAATTAAGATGCTCTTCAGGACAAAT 595  
Qy 495 CACTTTATCTGCTCATGGAATATCAGCTGAGGGGACTTGTGCTGCTCACTTTTGAATAGA 554  
Db |||||  
596 CACTTTATCTGCTCATGGAATATCAGCTGAGGGGACTTGTGCTGCTCACTTTTGAATAGA 655  
Qy 555 TATGAGGACCAAGTATGATGAAAACCTGATACAGTTTACCTAGCTGAGTGTGCTTGGCT 614  
Db |||||  
656 TATGAGGACCAAGTATGATGAAAACCTGATACAGTTTACCTAGCTGAGTGTGCTTGGCT 715  
Qy 615 GTTTCAGAGGTTTCATCTGATGGATACGTGTCATCAAGCTTCAGAGCTTCAGACATTTCTC 674  
Db |||||  
716 GTTTCAGAGGTTTCATCTGATGGATACGTGTCATCAAGCTTCAGAGCTTCAGACATTTCTC 775  
Qy 675 GTTGACCGCACAGGACACATCAAGCTGTTGGATTTTGGATCTGCCCGGAAAATGAATTCA 734  
Db |||||  
776 GTTGACCGCACAGGACACATCAAGCTGTTGGATTTTGGATCTGCCCGGAAAATGAATTCA 835  
Qy 735 AACAGATGGTGAATGCCAAACTCCCGATTTGGGACCCAGATTAATGCTCTCTGAAGTG 794  
Db |||||  
836 AACAGATGGTGAATGCCAAACTCCCGATTTGGGACCCAGATTAATGCTCTCTGAAGTG 895  
Qy 795 CTGACTGTGATGAACGGGGATGGAAGGACCTACGGCTGCACTGCTGCTGCTGCTCA 854  
Db |||||  
896 CTGACTGTGATGAACGGGGATGGAAGGACCTACGGCTGCACTGCTGCTGCTGCTCA 955  
Qy 855 GTGGGCGTGAATGCTCTATGAGATGATTTATGGAGATCCCTTTCGAGAGGAACTCT 914  
Db |||||  
956 GTGGGCGTGAATGCTCTATGAGATGATTTATGGAGATCCCTTTCGAGAGGAACTCT 1015  
Qy 915 GCCAGAACCTTCAATAACATTATGAATTTCCAG 947  
Db |||||  
1016 GCCAGAACCTTCAATAACATTATGAATTTCCAG 1048

RESULT 3  
US-10-450-763-29273  
; Sequence 29273, Application US/10450763  
; GENERAL INFORMATION:

APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 29273  
; LENGTH: 1830  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (1350)..(1640)  
; OTHER INFORMATION: 31% homologous to Homo sapiens Human myotonic dystrophy gene  
; OTHER INFORMATION: protein, accession number R41001, Smith-Waterman Score=77.  
US-10-450-763-29273

Query Match 15.2%; Score 225.6; DB 7; Length 1830;  
Best Local Similarity 54.0%; Pred. No. 5.9e-50;  
Matches 534; Conservative 0; Mismatches 439; Indels 15; Gaps 3;  
  
QY 184 CTGCTCTGATGAGATTAAAGCAGCTGAGCAACTTTGTCGGAGAGTATTCGACACCATAG 243  
DB 116 CGAACTGGCCCGGAGCAAGTAGCTGGCCGACTTTTGCAGTGGCGGAGCCCATCGTG 175  
  
QY 244 CTGAGTTACAGGAGCTCCAGCTTCCGCAAGAGACTTTCGAAGTCAGAGTCTTGTTAGGTT 303  
DB 176 TGAGGCTTAAGAGGTCGCGACTCCAGAGGACGACTTCGAGATCTGAGGTGATCGGAC 235  
  
QY 304 GTGGTCACCTTTGCTGAAGTCAGGTGGTAAAGAGAAAGCAACCGGGGACATCTATGCTA 363  
DB 236 GCGGGCGCTTACGAGAGGTAGCGGTAGTGAAGATGAAGCAGACGCGGCGGAGTATGCCA 295  
  
QY 364 TGAAGTGTATGAGAGAGAGGCTTTATTTGGCCAGGAGGAGGTTTCATTTTGGAGGAG 423  
DB 296 TGAAGATCATGAACAAAGTGGGACATCTGAAGAGGGGCGAGGTGTCGTCTCCGTGAGG 355  
  
QY 424 AGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCTTTTC 483  
DB 356 AGAGGAGCGTGTGGTGAATGGGGACCGGGGTGGATCAGCAGCTGCATCTCGCTTCC 415  
  
QY 484 AGGACAAAATACCTTTTATCTGGTCATGGAATATCAGCCTGAGGGGAGCTTGTCTGTAC 543  
DB 416 AGGATGAGAACTACCTGTACTTGGTCATGGAGTATTACGTGGGCGGGGACCTGCTGACAC 475  
  
QY 544 TTTTGAATAGATATGAGGACAGTTAGATGAACACCTGTATACGTTTACCTAGCTGAGC 603  
DB 476 TCGTAGCAAGTTTGGGGAGCGGATTCGCGCCGAGATGGCGGCTTCTACCTGGCGGAGA 535  
  
QY 604 TGAATTTGGCTGTTCACAGCGTTTCATCTGATGGATACGTGTCATCGAGACATCAAGCCGTG 663  
DB 536 TTGTCATGGCCATAGACTCGGTGCACCGGCTTGGCTAGCTGTCACAGGACATCAACCCG 595  
  
QY 664 AGAACAATTCCTGTTGACCGCAGGACACATCAAGCTGGTGGATTTTGGATCTGCGCGGA 723  
DB 596 ACAACATCTGCTGGACCGCTGTGGCCACATCCGCTGGCCGACTTCGGCTCTTGCTCA 655  
  
QY 724 AATGAATTCACAAGATGGTGAATGCCAACTCCCGATTGGGACCCCGAGATTAATGG 783  
DB 656 AGCTGCGGGCAGATGGAACGCTGCGGTGCTGCTGGTGGCTGTGGGACCCCGAGACTACCTGT 715  
  
QY 784 CTCTCAAGTGTGA ---CTGTGATGAACGCGGATGGAAGGACCTACGGGCTGACT 840  
DB 716 CCCCCAGATCTTCGAGGCTGTGGGCGGTGGCGCTGGGACAGCAGCTACGGGCGCCGAGT 775  
  
QY 841 GTGACTGGTGTGAGTGGGCGGTGATTTGCCTATGAGATGATTTTATGGGAGATCCCCCTTCG 900

DB 776 GTGACTGGTGGCGCTGGGTGTATTGCGCTATGAAATGTTCTATGGGACAGACGCCCTTCT 835  
QY 901 CAGAGGGAACCTCTGCGCAGAACCTTCAATAACATTATGATTTCCAGCGGTTTTTGAAT 960  
DB 836 ACAGGATTCACCGCGGAGACCTATGGCAAGATCTGCTCACTAAGAGACACTCTCTC 895  
QY 961 TTCCAGATGACCCCAAAAGTGAGCAGT---GACTTTTCTTGATCTGTATTCAAAGCTTGTGT 1017  
DB 896 TGCCGCTGTGGAGCAAGGGGTCCTGAGGAGGCTCGAGACTTCATTACGCGGTGCTGT 955  
QY 1018 GCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTTGTGTC-----CATCTTTTCT 1068  
DB 956 GTCCCCCGGAGACACGCTGGCGCGGTGGAGCGGACTTCCGAGACATCCCTTCT 1015  
QY 1069 TCTCTAAATTTGACTGGAACAACATTGTAACCTCTCTCCCTCCCTTCGTTCCACCCCTCA 1128  
DB 1016 TCTTTGGCTCTGACTGGATGGTCTCCGGAGAGCGTGGCCCCCTTTACACCGGATTCG 1075  
QY 1129 AGTCCGACGATGACACCTCCAAATTTTGA 1156  
DB 1076 AAGTGCCACCGACACATCAACTTGA 1103

RESULT 4  
US-10-450-763-21232  
; Sequence 21232, Application US/10450763  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 21232  
; LENGTH: 6303  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (3137)..(5767)  
; OTHER INFORMATION: 79% homologous to Homo sapiens Human myotonic dystrophy gene  
; OTHER INFORMATION: protein, accession number R41001, Smith-Waterman Score=3811.  
US-10-450-763-21232

Query Match 15.2%; Score 225.6; DB 7; Length 6303;  
Best Local Similarity 54.0%; Pred. No. 8.4e-50;  
Matches 534; Conservative 0; Mismatches 439; Indels 15; Gaps 3;  
  
QY 184 CTGCTCTGATGAGATTAAAGCAGCTGAGCAACTTTGTCGGAGAGTATTCGACACCATAG 243  
DB 3788 CGAACTGGCCCGGAGCAAGTAGCTGGCCGACTTTTGCAGTGGCGGAGCCCATCGTG 3847  
  
QY 244 CTGAGTTACAGGAGCTCCAGCTTCCGCAAGAGACTTCGAAAGTCAGAAAGTCTTGTAGGTT 303  
DB 3848 TGAGGCTTAAGGAGGTCGACTTCGAGGAGGACGACTTCGAGATCTTGAAGTGTATCGGAC 3907  
  
QY 304 GTGGTCATTTGCTGAAGTGCAGGTGGTAAAGAGAGAAAGCAACCGGGGACATCTATGCTA 363  
DB 3908 GCGGGCGCTTACGCGGAGGTAGCGGTAGTGAAGATGAAGCAGACGCGGCGGAGTATGCCA 3967  
  
QY 364 TGAAGTGTATGAAGAGAGGCTTTTATTCGCCCCAGGAGCAGGTTTCATTTTGGAGGAG 423  
DB 3968 TGAAGATCATGAACAAAGTGGGACATCTGTAAGAGGGGCGGAGGTGTCGTCTCCGTGAGG 4027  
  
QY 424 AGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCTTTC 483



Db 979 CGGTGGGGCAGAAATGGAATAGAGGATTTCAAAAGACATCGGTTTTTGAAGGTCTAAAT 1038  
Qy 1083 TGGAAACAATTCGTAACTCTCTCCCTCCCTTCGTTCCCAACCTCAAGTCGACGATGAC 1142  
Db 1039 TGGGAAATATACAAACCTAGAGACCTTATATTCCTGATGTGACGATCTCTCTGAC 1098  
Qy 1143 ACCTCAATTTTGTATGAACACAGAGAGAAATTCGTGGGTTTCATCTCTCGTCCGACGCTG 1202  
Db 1099 ACATCAACTTCGACGTGGATGACGACGTCTGAGAAACACCGGAAATATTTACCTCTCTGGT 1158  
Qy 1203 AGCCCTCAGGCTCTCGGTGAGAACTGCGCTTTGTGGGTTTGTGATCAGCAAGGCA 1262  
Db 1159 TCTCACACAGGCTTTTCTGATTAACATTTGCCATTATGTTGTTTACATTTCAACACGAA 1218  
Qy 1263 CTGGGATTTCTGGTAGA 1280  
Db 1219 AGCTGTTTCTGATCGA 1236

RESULT 6

PCT-US03-11189-11  
; Sequence 11, Application PC/TUS0311189  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE  
; FILE OF INVENTION: POLYPEPTIDE, BMSNKC\_0020/0021  
; FILE REFERENCE: D0193 PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/11189  
; CURRENT FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: U.S. 60/372,745  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 204  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US03-11189-11

Query Match 13.7%; Score 202.4; DB 1; Length 204;  
Best Local Similarity 99.5%; Pred. No. 4.5e-44;  
Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 744 GTGAATGCCAAATCCCGATTGGGACCCCAAGATTACATGGCTCTCGAAGTGTGACTGTG 803  
Db 1 GTGAATGCCAAATCCCGATTGGGACCCCAAGATTACATGGCTCTCGAAGTGTGACTGTG 60  
Qy 804 ATGAACGGGGATGGAAGAACGACCTACGGCTGGACTGTGACTGTGTTGGTCAAGTGGCGGTG 863  
Db 61 ATGAACGGGGATGGAAGAACGACCTACGGCTGGACTGTGACTGTGTTGGTCAAGTGGCGGTG 120  
Qy 864 ATGGCTATGAGATGATTTATGGAGATCCCTTCGAGAGGAACTCTGCCAAGCC 923  
Db 121 ATGGCTATGAGATGATTTATGGAGATCCCTTCGAGAGGAACTCTGCCAAGCC 180  
Qy 924 TTCAATAACATTAATGAATTTCCAG 947  
Db 181 TTCAATAACATTAATGAATTTCCAG 204

RESULT 7

PCT-US04-42360-13  
; Sequence 13, Application PC/TUS0442360  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
; APPLICANT: Hospital / Bayer AG  
; TITLE OF INVENTION: Nucleotide sequences involved in pain  
; FILE REFERENCE: 17633/2048  
; CURRENT APPLICATION NUMBER: PCT/US04/42360  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: 60/531,341  
; PRIOR FILING DATE: 19-Dec-2003  
; NUMBER OF SEQ ID NOS: 2587

; SOFTWARE: Perl script  
; SEQ ID NO 13  
; LENGTH: 5333  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Refseq / NM\_053620  
; DATABASE ENTRY DATE: 2003-10-05  
PCT-US04-42360-13

Query Match 13.2%; Score 196; DB 1; Length 5333;  
Best Local Similarity 49.5%; Pred. No. 5.5e-42;  
Matches 573; Conservative 0; Mismatches 570; Indels 15; Gaps 2;  
Qy 135 GAAGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGACAGTCAGCTGCTCTGATG 194  
Db 130 GAGACCTGTGGACGTGTGTTGTTGCTTTTACACGAGTGCAGCACCTCGGGCTCGGC 189  
Qy 195 AAGATTAAAGCAGTGAAGCACTTTGTCGGAGTATTTCCGACACCATATAGCTGAGTTACAG 254  
Db 190 CGCGACAAGTATGTGGCGAGTTCTCGAGTGGCTAAGCCATTACCCAGCTCGTGAAG 249  
Qy 255 GAGCTCCAGCTTCGGCAAGAGACTTCGAGTCAAGTCTTGTAGTTGTGTGTCATTTT 314  
Db 250 GACATGCACTTCATCGGGAGGACTTTGAGATCATCAAAAGTGTATGGAAGAGGAGCTTTT 309  
Qy 315 GCTGAAGTCCAGTGTGAAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTGTATG 374  
Db 310 GGTGAGTTGCTGTTGTTCAAAATGAAGAACACTGAACGAATTTATGCAATGAAATTTCTC 369  
Qy 375 AAGAAGAAGGCTTTATTTGGCCAGGAGCAGGTTTCTATTTTGGAGAAAGACCGGAAACATA 434  
Db 370 AACAAATGGAGATGCTAAGAGAGCAGACAGCTTGTCTTCGAGAGAGAGGGATGTG 429  
Qy 435 TTATCTCGAAGCACAAAGCCCGTGGATCCCAATTAAGTATGCTCTTTCAGGACAAAAAT 494  
Db 430 CTGGTGAACGCTGACTGCCAGTGGATCACTGCGCTACACTACGCCCTTTCAAGATGGAAC 489  
Qy 495 CACCTTTATCTGTCATGAATATATCAGCTGGAGGGGACTGCTGTCACCTTTTGAATAGA 554  
Db 490 TACCTGTATTTGTTATGATTAATCTATGTTGGTGGTGGTGTGCTGTGACCTCTGCTGAGTAAG 549  
Qy 555 TATGAGGACCACTTAGATGAAAACCTGTATACAGTTTTTACCTAGCTGAGCTGATTTTGGCT 614  
Db 550 TTTGAAGACAAATCTCCAGAGCATGGCGAGTTCTACATTGGCGAGATGGTGTGGCC 609  
Qy 615 GTTCAAGCGTTTCATCTGATGGGATACGTGTCATCGAGATCAATCAAGCTCGAGAACTTCTC 674  
Db 610 ATCGACTCGATCCACCGCTCCACTATGTGTCACAGAGACATTAACCCGACAAACGCTCTT 669  
Qy 675 GTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCCGGAAATGAATTCA 734  
Db 670 CTGGATGTCAACGGTCAATCCGCTGGCTGCTGACTTTTGGCTCGTGTGAGATGAACGAT 729  
Qy 735 AACCAAGATGCTGAATGCCAAACTCCCGATTGGGACCCCAAGATTACATGGCTCTCTGAAGTG 794  
Db 730 GACGGCACTGTTCACTTCCGTTGGCTGGGACACACTGACTACATCTCACCAGAGATC 789  
Qy 795 CTGACTGTGATGAACGGGGATGGAAGGACCTACGGCTCGGACTGTGACTGCTGGTGTCA 854  
Db 790 CTGACGGCCATG---GAGGATGGCATGGGCAAAATACGGGCCCGAGTGCAGCTGGTGGTCC 846  
Qy 855 GTGGGGGTGATTTGCTTATGAGATGATTTATGGAGATCCCTTCGACAGGGAACCTCTCT 914  
Db 847 CTGGGGGTCTGATGTATGAGATGCTGTATGAGAAACGCCATTTTATGACAGATCTCTG 906  
Qy 915 GGCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAATTTTCCA----- 965  
Db 907 GTGGAGACATATGGAAGAGATCATGAACACGAGGAGCGGTTTCAGTTCCCATCCACGTC 966  
Qy 966 ----GATGACCCCAAGTGAAGTGTGACTTTTGTGATCTGATTCATAAGCTTTGTGTGGGC 1022  
Db 967 ACTGACGTCTCTGAAGAAGCGAAAGACCTCATCCAGAGACTAATATGACAGAGAGCGC 1026



; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1334  
; LENGTH: 489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-060-756-1334

Query Match 11.6%; Score 171.8; DB 8; Length 489;  
Best Local Similarity 98.9%; Pred. No. 7.2e-36;  
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1102 CTCCTCCCTCCCTTCGTTCCACCCCTCAAGTCCGACGATGACACCTCCAAATTTTGATGAAC 1161  
DB 315 CTCCTCCCTCCCTTCGTTCCACCCCTCAAGTCTGACGATGACACCTCCAAATTTTGATGAAC 374  
  
QY 1162 CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGG 1221  
DB 375 CAAAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGG 434  
  
QY 1222 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGGCACTGGGGATTCCTGG 1276  
DB 435 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGGCACTGGGGATTCCTGG 489

RESULT 11  
US-11-060-756-1335  
; Sequence 1335, Application US/11060756  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1335  
; LENGTH: 489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-060-756-1335

Query Match 11.6%; Score 171.8; DB 8; Length 489;  
Best Local Similarity 98.9%; Pred. No. 7.2e-36;  
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1102 CTCCTCCCTCCCTTCGTTCCACCCCTCAAGTCCGACGATGACACCTCCAAATTTTGATGAAC 1161  
DB 315 CTCCTCCCTCCCTTCGTTCCACCCCTCAAGTCTGACGATGACACCTCCAAATTTTGATGAAC 374  
  
QY 1162 CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGG 1221  
DB 375 CAAAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGG 434  
  
QY 1222 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGGCACTGGGGATTCCTGG 1276  
DB 435 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGGCACTGGGGATTCCTGG 489

RESULT 12  
US-11-060-756-5606  
; Sequence 5606, Application US/11060756  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756

; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5606  
; LENGTH: 489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-060-756-5606

Query Match 11.6%; Score 171.8; DB 8; Length 489;  
Best Local Similarity 98.9%; Pred. No. 7.2e-36;  
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1102 CTCCTCCCTCCCTTCGTTCCACCCCTCAAGTCCGACGATGACACCTCCAAATTTTGATGAAC 1161  
DB 315 CTCCTCCCTCCCTTCGTTCCACCCCTCAAGTCTGACGATGACACCTCCAAATTTTGATGAAC 374  
  
QY 1162 CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGG 1221  
DB 375 CAAAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGG 434  
  
QY 1222 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGGCACTGGGGATTCCTGG 1276  
DB 435 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGGCACTGGGGATTCCTGG 489

RESULT 13  
US-11-060-756-5607  
; Sequence 5607, Application US/11060756  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5607  
; LENGTH: 489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-060-756-5607

Query Match 11.6%; Score 171.8; DB 8; Length 489;  
Best Local Similarity 98.9%; Pred. No. 7.2e-36;  
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1102 CTCCTCCCTCCCTTCGTTCCACCCCTCAAGTCCGACGATGACACCTCCAAATTTTGATGAAC 1161  
DB 315 CTCCTCCCTCCCTTCGTTCCACCCCTCAAGTCTGACGATGACACCTCCAAATTTTGATGAAC 374  
  
QY 1162 CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGG 1221  
DB 375 CAAAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGG 434  
  
QY 1222 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGGCACTGGGGATTCCTGG 1276  
DB 435 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGGCACTGGGGATTCCTGG 489

RESULT 14  
PCT-US03-11189-9  
; Sequence 9, Application PC/TUS0311189  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE  
; FILE OF INVENTION: POLYPEPTIDE, BMSNKC\_0020/0021  
; FILE REFERENCE: D0193 PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/11189  
; CURRENT FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: U.S. 60/372,745

```
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 143
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-11189-9

Query Match          9.7%; Score 143; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.1e-28;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 GTCATGAATATCAGCCTGAGGGGACTTCTGCTCACTTTTGAATAGATATGAGGCCAG 566
Db 1 GTCATGAATATCAGCCTGAGGGGACTTCTGCTCACTTTTGAATAGATATGAGGCCAG 60
|||||
QY 567 TTAGATGAAACCTGATACAGTTTACCTAGCTGAGCTGATTTGGCTGTTACAGCGTT 626
Db 61 TTAGATGAAACCTGATACAGTTTACCTAGCTGAGCTGATTTGGCTGTTACAGCGTT 120
|||||
QY 627 CATCTGATGGGATACGTGCATCG 649
Db 121 CATCTGATGGGATACGTGCATCG 143
|||||

RESULT 15
PCT-US03-11189-6
; Sequence 6, Application PC/TUS0311189
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
; TITLE OF INVENTION: POLYPEPTIDE, BMSKNC_0020/0021
; FILE REFERENCE: D0193 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/11189
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: U.S. 60/372,745
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-11189-6

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Search completed: March 19, 2005, 17:43:23  
Job time : 349.017 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 07:57:47 ; Search time 5227.99 Seconds  
(without alignments)  
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Title: US-10-724-594-1\_COPY\_17\_1497

Perfect score: 1481

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Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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US-10-311-034-33

; Sequence 33, Application US/10311034

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: YUE, Henry

; APPLICANT: LAL, Preeti

; APPLICANT: BANDMAN, Olga

; APPLICANT: BOROWSKY, Mark L.

; APPLICANT: AU-YOUNG, Janice

; APPLICANT: LU, Yan

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: CHAWLA, Narinder K.

; APPLICANT: YAO, Monique G.

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: GREENWALD, Sara R.

; APPLICANT: RAMKUMAR, Javalaxmi

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: KEARNEY, Liam

; APPLICANT: BURFORD, Neil

; APPLICANT: NGUYEN, Danniell B.

; APPLICANT: TANG, Y. Tom  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: HE, Ann  
; APPLICANT: THORNTON, Michael  
; APPLICANT: HAPALIA, April  
; APPLICANT: ARVIZO, Chandra S.  
; APPLICANT: GURURAJAN, Rajagopal  
; APPLICANT: LO, Terence P.  
; APPLICANT: KHAH, Farrah A.  
; APPLICANT: RECIPON, Shirley A.  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: POLICKI, Jennifer L.  
; APPLICANT: DING, Li  
; APPLICANT: GREYER, Megan  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: BATRA, Sajeew  
; APPLICANT: ISON, Craig H.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0125 PCT  
; CURRENT APPLICATION NUMBER: US/10/311,034  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/215,605; 60/218,372;  
; 60/228,056  
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25  
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; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John A.  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Ju, Jingfang  
; APPLICANT: Li, Li  
; APPLICANT: Guo, Xiaojia (Sasha)  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Ort, Tatiana  
; APPLICANT: Gorman, Linda  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Catterton, Elina  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Stone, David J.  
; APPLICANT: Pena, Carol E. A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Rothenberg, Mark E.  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Agee, Michele L.  
; APPLICANT: Berghs, Constance  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-462C  
; CURRENT APPLICATION NUMBER: US/10/262,511  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: 60/326,483  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: 60/373,815  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/327,917  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/381,642  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/328,029  
; PRIOR FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: 60/381,038  
; PRIOR FILING DATE: 2002-05-16  
; PRIOR APPLICATION NUMBER: 60/328,056  
; PRIOR FILING DATE: 2001-10-09



APPLICANT: Shenoy, Suresh G.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Rothenberg, Mark E.  
APPLICANT: Leach, Martin D.  
APPLICANT: Agee, Michele L.  
APPLICANT: Berghs, Constance  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-462C  
CURRENT APPLICATION NUMBER: US/10/262,511A  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: 60/326,483  
PRIOR FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: 60/373,815  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: 60/327,917  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/381,642  
PRIOR FILING DATE: 2002-05-17  
PRIOR APPLICATION NUMBER: 60/328,029  
PRIOR FILING DATE: 2002-10-09  
PRIOR APPLICATION NUMBER: 60/381,038  
PRIOR FILING DATE: 2002-05-16  
PRIOR APPLICATION NUMBER: 60/328,056  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/373,260  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: 60/373,826  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: 60/327,435  
PRIOR FILING DATE: 2001-10-05  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 439  
SOFTWARE: Curasequid version 0.1  
SEQ ID NO 3  
LENGTH: 1870  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2)...(1870)  
US-10-262-511A-3

Query Match 93.7%; Score 1388.2; DB 51; Length 1870;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	TCAAATATGAGCGCGGAATCTTTGGATGCTGCTGCTGAACCCATTGCCAGCGGG	60
Db	24	TCAAATATGAGCGCGGAATCTTTGGATGCTGCTGCTGAACCCATTGCCAGCGGG	83
Qy	61	CTCCAGGCTGAATCTCTTCCAGGGGAACACCCCTTTATGACTCAACAGCAGATGT	120
Db	84	CTCCAGGCTGAATCTCTTCCAGGGGAACACCCCTTTATGACTCAACAGCAGATGT	143
Qy	121	CTCTCTTTCCGAGAAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC	180
Db	144	CTCTCTTTCCGAGAAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC	203
Qy	181	AGCGTCTCTGATGAAGATTAAGCACGTGACAACTTTGTCCGGAAGTATTCGACACCA	240
Db	204	AGCGTCTCTGATGAAGATTAAGCACGTGACAACTTTGTCCGGAAGTATTCGACACCA	263
Qy	241	TAGCTGATTTACAGGACTCCAGCTTCCGGAAGGACTTCGAAGTCAAGTCTTGATG	300
Db	264	TAGCTGATTTACAGGACTCCAGCTTCCGGAAGGACTTCGAAGTCAAGTCTTGATG	323
Qy	301	GTTGTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAGAAGCAACCGGGGACATCTATG	360
Db	324	GTTGTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAGAAGCAACCGGGGACATCTATG	383
Qy	361	CTATGAAGTATGAAGAAGGCTTTATTTGGCCAGGAGCAGGTTTCATTTTGGAGG	420
Db	384	CTATGAAGTATGAAGAAGGCTTTATTTGGCCAGGAGCAGGTTTCATTTTGGAGG	443

Qy	421	ARGAGCGGACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTACAGTATGCCT	480
Db	444	ARGAGCGGACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTACAGTATGCCT	503
Qy	481	TTCAGGACAAAAATCACCTTTATCTGGTCAATGAATATCAGCCTCGAGGGGACTTGTGT	540
Db	504	TTCAGGACAAAAATCACCTTTATCTGGTCAATGAATATCAGCCTCGAGGGGACTTGTGT	563
Qy	541	CACCTTTGAATAGATATGAGGACAGTTAGATGAAAACTTGATACAGTTTTCAGTCTG	600
Db	564	CACCTTTGAATAGATATGAGGACAGTTAGATGAAAACTTGATACAGTTTTCAGTCTG	623
Qy	601	AGCTGATTTTGGCTGTTCAAGGTTTCACTGTATGGATACGTGATCGAGACATCAAGC	660
Db	624	AGCTGATTTTGGCTGTTCAAGGTTTCACTGTATGGATACGTGATCGAGACATCAAGC	683
Qy	661	CTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG	720
Db	684	CTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG	743
Qy	721	CGAAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTTGGGACCCCAAGTACA	780
Db	744	CGAAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTTGGGACCCCAAGTACA	803
Qy	781	TGGCTCTGAGCTGCTGATGATGAACGGGGATGGAAGGACCTACGGCCTGGACT	840
Db	804	TGGCTCTGAGCTGCTGATGATGAACGGGGATGGAAGGACCTACGGCCTGGACT	863
Qy	841	GTGACTGGTGGTCAAGTGGGCGTATTCCTATGAGATGATTTATGGAGATCCCCCTTCG	900
Db	864	GTGACTGGTGGTCAAGTGGGCGTATTCCTATGAGATGATTTATGGAGATCCCCCTTCG	923
Qy	901	CAGAGGGAACCTCTGCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAT	960
Db	924	CAGAGGGAACCTCTGCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAT	983
Qy	961	TTCCAGATGACCCCAAGTGAGCAGTGACTTTCTGATCTGATTTCAAGCTCTGTGCG	1020
Db	984	TTCCAGATGACCCCAAGTGAGCAGTGACTTTCTGATCTGATTTCAAGCTCTGTGCG	1043
Qy	1021	GCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGTGCGCATCCTTTCTTTCTTAAATTTG	1080
Db	1044	GCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGTGCGCATCCTTTCTTTCTTAAATTTG	1103
Qy	1081	ACTGGAACAACATTCGTAACTCTCTCCCGCTTGTGTTCCACCCCTCAAGTCCGACATG	1140
Db	1104	ACTGGAACAACATTCGTAACTCTCTCCCGCTTGTGTTCCACCCCTCAAGTCTGACGATG	1163
Qy	1141	ACACCTCCCAATTTTGTATGAACCAAGAGAAATTCGTGGGTTTTCATCTCTCCGTGCCAGC	1200
Db	1164	ACACCTCCCAATTTTGTATGAACCAAGAGAAATTCGTGGGTTTTCATCTCTCCGTGCCAGC	1223
Qy	1201	TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTTGTACAGCAAGG	1260
Db	1224	TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTTGTACAGCAAGG	1283
Qy	1261	CACCTGGGATCTTGTGTAGATCTGATCTGTGTGTGCGGTCTGAGACTCCCTCCCAAGA	1320
Db	1284	CACCTGGGATCTTGTGTAGATCTGATCTGTGTGTGCGGTCTGAGACTCCCTCCCAAGA	1343
Qy	1321	CTAGCTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTTACAGACTCTCAGACA	1380
Db	1344	CTAGCTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTTACAGACTCTCAGACA	1403
Qy	1381	AGTGTCACAAGGT 1393	
Db	1404	AGTGTCACAAGAT 1416	

RESULT 7  
US-10-791-666-3  
; Sequence 3, Application US/10791666



[illegible]



;; PRIOR FILING DATE: 2000-11-16  
;; PRIOR APPLICATION NUMBER: US 60/252,730  
;; PRIOR FILING DATE: 2000-11-22  
;; PRIOR APPLICATION NUMBER: US 60/250,807  
;; PRIOR FILING DATE: 2000-12-01  
;; NUMBER OF SEQ ID NOS: 44  
;; SOFTWARE: PERL Program  
;; SEQ ID NO 43  
;; LENGTH: 6298  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; OTHER INFORMATION: Incyte ID No: 7484498CB1  
US-10-415-011-43

Query Match 93.7%; Score 1388.2; DB 54; Length 6298;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TCAATATGAGCGCGGAATCTTTGGATGCTGGTCTGCTGAACCCATTGCCAACCGGG 60  
DB 65 TCAATATGAGCGCGGAATCTTTGGATGCTGGTCTGCTGAACCCATTGCCAACCGGG 124  
QY 61 CTTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCCCTTTATGACTCAACAGCAGATGT 120  
DB 125 CTTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCCCTTTATGACTCAACAGCAGATGT 184  
QY 121 CTCTCTTTCCGAGAGGATATTAGATGCCCTCTTTGTTCTTTTGAAGATGCAGTC 180  
DB 185 CTCTCTTTCCGAGAGGATATTAGATGCCCTCTTTGTTCTTTTGAAGATGCAGTC 244  
QY 181 AGCTGCTCTGATGAAGATTAAAGCAGTGAAGCAACTTTTGCCGGAAGTATTTCGACACCA 240  
DB 245 AGCTGCTCTGATGAAGATTAAAGCAGTGAAGCAACTTTTGCCGGAAGTATTTCGACACCA 304  
QY 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGCAAGGACTTCGAAAGTCAGAGTCTTTGTAG 300  
DB 305 TAGCTGAGTTACAGGAGCTCCAGCCTTCGCAAGGACTTCGAAAGTCAGAGTCTTTGTAG 364  
QY 301 GTTGTGTCATCTTGTGAAGTCCAGTGTGATGAGAGAGAGCAACCGGGGACATCTATG 360  
DB 365 GTTGTGTCATCTTGTGAAGTCCAGTGTGATGAGAGAGAGCAACCGGGGACATCTATG 424  
QY 361 CTATGAAGTGAATGAAGAGAGGCTTTATTGCGCCAGGAGCAGGTTTCAATTTTGGAG 420  
DB 425 CTATGAAGTGAATGAAGAGAGGCTTTATTGCGCCAGGAGCAGGTTTCAATTTTGGAG 484  
QY 421 AAGAGCGGAACATATTATCTCGAAGCACAGCCCGTGGATCCGCCCAATTAAGTATGCCT 480  
DB 485 AAGAGCGGAACATATTATCTCGAAGCACAGCCCGTGGATCCGCCCAATTAAGTATGCCT 544  
QY 481 TTGAGCAAAATATCACTTTATCTGTCATGGAATATCAGCTGAGGGGACTTCTGT 540  
DB 545 TTGAGCAAAATATCACTTTATCTGTCATGGAATATCAGCTGAGGGGACTTCTGT 604  
QY 541 CACTTTTGAATAGATGAGGACAGTATGATCAAAACCTGTATACAGTCTTACCTAGCTG 600  
DB 605 CACTTTTGAATAGATGAGGACAGTATGATCAAAACCTGTATACAGTCTTACCTAGCTG 664  
QY 601 AGCTGATTTTGGCTGTTCACAGCGTTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660  
DB 665 AGCTGATTTTGGCTGTTCACAGCGTTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 724  
QY 661 CTGAGAACATCTCTGTTGACCGCACAGGACACATCAAGCTGTGGATTTTGGATCTGCCG 720  
DB 725 CTGAGAACATCTCTGTTGACCGCACAGGACACATCAAGCTGTGGATTTTGGATCTGCCG 784  
QY 721 CGAAATGAATTCAAACAGATGCTGAATGCCAAACTCCCGATTGGGACCCAGATTACA 780  
DB 785 CGAAATGAATTCAAACAGATGCTGAATGCCAAACTCCCGATTGGGACCCAGATTACA 844  
QY 781 TGGCTCTCGAAGTGTGCTGATGAAACCGGGGATGAAAGGCACTACGGCTCGGACT 840

DB 845 TGGCTCTCGAAGTGTGCTGATGAAACCGGGATGAAAGGCACTACGGCTCGGACT 904  
QY 841 GTGACTGGTGGTTCAGTGGCGGTGATTGCTTATGAGATGATTTATGGAGATCCCTTCG 900  
DB 905 GTGACTGGTGGTTCAGTGGCGGTGATTGCTTATGAGATGATTTATGGAGATCCCTTCG 964  
QY 901 CAGAGGGAACCTCTGCGCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTGAAAT 960  
DB 965 CAGAGGGAACCTCTGCGCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTGAAAT 1024  
QY 961 TTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATCTGAATCAAGCTTTGTGCG 1020  
DB 1025 TTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATCTGAATCAAGCTTTGTGCG 1084  
QY 1021 GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTGTGCGCACTCTTCTCTCTAAAATG 1080  
DB 1085 GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTGTGCGCACTCTTCTCTCTAAAATG 1144  
QY 1081 ACTGGAACCAACATTCGTAATCTCTCTCCCTCCCTTCGTTCCACCTCAAGTCCGACGATG 1140  
DB 1145 ACTGGAACCAACATTCGTAATCTCTCTCCCTCCCTTCGTTCCACCTCAAGTCTGACGATG 1204  
QY 1141 ACACCTCCAAATTTTGAAGAACAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1200  
DB 1205 ACACCTCCAAATTTTGAAGAACAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1264  
QY 1201 TGAGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAG 1260  
DB 1265 TGAGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAG 1324  
QY 1261 CACTGGGATTTCTGTTAGATCTGAGTCTGTTGTGCGGTCTGGACTCCCTGCCAAGA 1320  
DB 1325 CACTGGGATTTCTGTTAGATCTGAGTCTGTTGTGCGGTCTGGACTCCCTGCCAAGA 1384  
QY 1321 CTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1380  
DB 1385 CTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1444  
QY 1381 AGTGTCAACAGCT 1393  
DB 1445 AGTGTCAACAGAT 1457

RESULT 10  
US-10-170-235-7679  
; Sequence 7679, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
; TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF  
; FILE REFERENCE: CL001380  
; CURRENT APPLICATION NUMBER: US/10/170,235  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 42514  
; SEQ ID NO 7679  
; LENGTH: 8602  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-7679

Query Match 93.7%; Score 1388.2; DB 49; Length 8602;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TCAATATGAGCGCGGAATCTTTGGATGCTGGTGTCTGCTGAACCCATTGCCAACCGGG 60  
DB 67 TCAATATGAGCGCGGAATCTTTGGATGCTGGTGTCTGCTGAACCCATTGCCAACCGGG 136  
QY 61 CTTCCAGGCTGAATCTGTTCTTCAGGGGAAACCCCTTTATGACTCAACAGCAGATGT 120  
DB 127 CTTCCAGGCTGAATCTGTTCTTCAGGGGAAACCCCTTTATGACTCAACAGCAGATGT 186

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QY 121 CTCCTCTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAAATGCAGTC 180
DB 187 CTCCTCTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAAATGCAGTC 246
QY 181 AGCTGCTCTGATGAAGATTAAAGCAGTGAGCAACTTTGTCGGGAAGTATTCCGACACCA 240
DB 247 AGCTGCTCTGATGAAGATTAAAGCAGTGAGCAACTTTGTCGGGAAGTATTCCGACACCA 306
QY 241 TAGCTGATTACAGGAGCTCCAGCTTCCGCAAGGACTTCGAAGTCAGAGTCTTGATG 300
DB 307 TAGCTGATTACAGGAGCTCCAGCTTCCGCAAGGACTTCGAAGTCAGAGTCTTGATG 366
QY 301 GTTGTGTCACCTTTGCTGAGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 360
DB 367 GTTGTGTCACCTTTGCTGAGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 426
QY 361 CTATGAAGTATGAAGAAAGGCTTTTATGCGCCAGGAGCAGTTTCAATTTTGAAG 420
DB 427 CTATGAAGTATGAAGAAAGGCTTTTATGCGCCAGGAGCAGTTTCAATTTTGAAG 486
QY 421 AAGAGCGGACATATTATCTCGAGCAGCAAGCCCGTGGATCCCCCAATTACAGTATGCCT 480
DB 487 AAGAGCGGACATATTATCTCGAGCAGCAAGCCCGTGGATCCCCCAATTACAGTATGCCT 546
QY 481 TTCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCTCGAGGGGACTTGTGT 540
DB 547 TTCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCTCGAGGGGACTTGTGT 606
QY 541 CACTTTTGAATAGATAGAGACCAAGTATAGATGAAGAAACCTGATACATTTTACCTAGCTG 600
DB 607 CACTTTTGAATAGATAGAGACCAAGTATAGATGAAGAAACCTGATACATTTTACCTAGCTG 666
QY 601 AGCTGATTTTGGCTGTTTCAGAGCTTTCATCTGATGGATAGCTGATCGAGACATCAAGC 660
DB 667 AGCTGATTTTGGCTGTTTCAGAGCTTTCATCTGATGGATAGCTGATCGAGACATCAAGC 726
QY 661 CTGAGAACATTTCTCGTTGACCGCAGCAGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
DB 727 CTGAGAACATTTCTCGTTGACCGCAGCAGACACATCAAGCTGGTGGATTTTGGATCTGCCG 786
QY 721 CGAAATATGAATTTCAAAACAAGATGTGAATGCAAACTCCCGATTTGGACCCCAAGATTACA 780
DB 787 CGAAATATGAATTTCAAAACAAGATGTGAATGCAAACTCCCGATTTGGACCCCAAGATTACA 846
QY 781 TGGCTCTGAGTCTGACTCTGATGAACCGGGATGAAAGGACCACTTACGGCTGAGCT 840
DB 847 TGGCTCTGAGTCTGACTCTGATGAACCGGGATGAAAGGACCACTTACGGCTGAGCT 906
QY 841 GTGACTGCTGATGAGTGGGCTGATTCCTATGAGATGATTTATGGAGATCCCCCTTCG 900
DB 907 GTGACTGCTGATGAGTGGGCTGATTCCTATGAGATGATTTATGGAGATCCCCCTTCG 966
QY 901 CAGAGGAAACCTTCGCAGAACCTTCAATTAACATTATGAATTTTCAGCGGTTTTTGAAT 960
DB 967 CAGAGGAAACCTTCGCAGAACCTTCAATTAACATTATGAATTTTCAGCGGTTTTTGAAT 1026
QY 961 TTCCAGATGACCCCAAGTGCAGTCACTTTCTGATCTGATTCGATTCAGAGCTTGTGCG 1020
DB 1027 TTCCAGATGACCCCAAGTGCAGTCACTTTCTGATCTGATTCGATTCAGAGCTTGTGCG 1086
QY 1021 GCCAGAAAGAGAGACTGAAAGTTTGAAGGTCTTTGCTGCCATCTCTTCTCTCAAAATTG 1080
DB 1087 GCCAGAAAGAGAGACTGAAAGTTTGAAGGTCTTTGCTGCCATCTCTTCTCTCAAAATTG 1146
QY 1081 ACTGGAAACAATTCGTAACCTCTCTCCCGCTTCGTTTCCACCCCTCAAGTCGAGCAATG 1140
DB 1147 ACTGGAAACAATTCGTAACCTCTCTCCCGCTTCGTTTCCACCCCTCAAGTCGAGCAATG 1206
QY 1141 ACACCTCCAAATTTTGAATGACCAAGAGAAATTCGTGGGTTTTCATCTCTCCGTGCCAGC 1200
DB 1207 ACACCTCCAAATTTTGAATGACCAAGAGAAATTCGTGGGTTTTCATCTCTCCGTGCCAGC 1266
QY 1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGCTTTGTGGGTTTTTTCGTACAGCAAGG 1260
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DB 1267 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTTGTACAGCAAG 1326
QY 1261 CACTGGGATCTTGGTAGATCTGAGTCTGTTGTGCGGTCTGGACTCCCTGCCAAGA 1320
DB 1327 CACTGGGATCTTGGTAGATCTGAGTCTGTTGTGCGGTCTGGACTCCCTGCCAAGA 1386
QY 1321 CTAGCTCCATGGAAAAGAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1380
DB 1387 CTAGCTCCATGGAAAAGAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1446
QY 1381 AGTGTCAACAAGT 1393
DB 1447 AGTGTCAACAAGT 1459

RESULT 11
US-10-017-216-3
; Sequence 3, Application US/10017216
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A Novel Human Myotonic Dystrophy Type Protein
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 6159
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-017-216-3

Query Match 93.3%; Score 1381.8; DB 46; Length 6159;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1386; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCAAAATATGAGAGCGCGGAATCTTTTGGATGCTGCTGCTGCTGAACCCATTTGCCAACCGGG 60
DB 11 TCAAAATATGAGAGCGCGGAATCTTTTGGATGCTGCTGCTGCTGAACCCATTTGCCAACCGGG 70
QY 61 CCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTATGACTCAACAGCAGATGT 120
DB 71 CCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTATGACTCAACAGCAGATGT 130
QY 121 CTCTCTTTTCCCGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAAATGCAGTC 180
DB 131 CTCTCTTTTCCCGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAAATGCAGTC 190
QY 181 AGCTGCTCTGATGAAGATTAAAGCAGTGAGCAACTTTGTCGGAAAGTATTCCGACACCA 240
DB 191 AGCTGCTCTGATGAAGATTAAAGCAGTGAGCAACTTTGTCGGAAAGTATTCCGACACCA 250
QY 241 TAGCTGATTACAGGAGCTCCAGCTTCCGCAAGGACTTCGAAGTCAGAGTCTTGATG 300
DB 251 TAGCTGATTACAGGAGCTCCAGCTTCCGCAAGGACTTCGAAGTCAGAGTCTTGATG 310
QY 301 GTTGTGCTCACTTTGCTGAAAGTCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 360
DB 311 GTTGTGCTCACTTTGCTGAAAGTCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 370
QY 361 CTATGAAGTATGAAGAAAGGCTTTTATGCGCCAGGAGCAGGTTTCAATTTTGAAG 420
DB 371 CTATGAAGTATGAAGAAAGGCTTTTATGCGCCAGGAGCAGGTTTCAATTTTGAAG 430
QY 421 AAGAGCGGACATATTATCTCGAGCAGCAAGCCCGTGGATCCCCCAATTACAGTATGCCT 480
DB 431 AAGAGCGGACATATTATCTCGAGCAGCAAGCCCGTGGATCCCCCAATTACAGTATGCCT 490
QY 481 TTCAGGACAAAATCACCTTTTATCTGCTCATGGAATATCAGCTCGAGGGGACTTGTGT 540
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QY 1081 ACTGGAACAATTCGTAACTCTCTCCCTCCCTTCGTTCCTCCACCTCAAGTCCGAGATG 1140  
DB 1091 ACTGGAACAATTCGTAACTCTCTCCCTCCCTTCGTTCCTCCACCTCAAGTCTGACGATG 1150  
QY 1141 ACACCTCCAAATTTGATGAACAGAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1200  
DB 1151 ACACCTCCAAATTTGATGAACAGAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1210  
QY 1201 TGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGG 1260  
DB 1211 TGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGG 1270  
QY 1261 CACTGGGATTTCTGTGATGATCTGAGTCTCTGTGTGGGTTCTGGACTCCCTGCCAAGA 1320  
DB 1271 CACTGGGATTTCTGTGATGATCTGAGTCTCTGTGTGGGTTCTGGACTCCCTGCCAAGA 1330  
QY 1321 CTAGCTCCATGGAAGAAATCTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1380  
DB 1331 CTAGCTCCATGGAAGAAATCTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1390  
QY 1381 AGTGTCAAGGT 1393  
DB 1391 AGTGTCAAGAT 1403

## RESULT 14

PCT-US02-41011-10  
; Sequence 10, Application PC/TUS0241011  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Rosenfeld, Julie Beth  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,  
; TITLE OF INVENTION: 32838,336 and 52908  
; FILE REFERENCE: MP101-294P1RNWOM  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/341,953  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 6574  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
PCT-US02-41011-10

Query Match 93.3%; Score 1381.8; DB 1; Length 6574;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1386; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 89 CTCTCAGGCTGATCTGTTCTCCAGGGGAACCCCTTATGATCTCAACAGCATGT 148  
QY 121 CTCTCTTTCCGAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGATGAGTC 180  
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QY 301 GTTGTGGTCACTTTGCTGAAGTGCAGTGGTAAAGAGAAAGCAACCGGGGACATCTATG 360  
DB 329 GTTGTGGTCACTTTGCTGAAGTGCAGTGGTAAAGAGAAAGCAACCGGGGACATCTATG 388  
QY 361 CTATGAAAGTGAAGAGAGAGGCTTTATTTGGCCAGGAGAGGTTTCAATTTTGGAG 420  
DB 389 CTATGAAAGTGAAGAGAGAGGCTTTATTTGGCCAGGAGAGGTTTCAATTTTGGAG 448  
QY 421 AAGAGCGGAACATATTTATCTCGAAGCAACAAGCCCGTGGATCCCCCAATTAACAGTATGCCT 480  
DB 449 AAGAGCGGAACATATTTATCTCGAAGCAACAAGCCCGTGGATCCCCCAATTAACAGTATGCCT 508  
QY 481 TTCAGGACAAAATCACTTTATCTGGTCAATGGAATATCAGCTGAGGGGACTTGTGT 540  
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DB 749 CGAAATGAAATTCAAACAAGATGGTGAATGCCAAACTCCCGATGGGACCCAGATTACA 808  
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QY 841 GTGACTGTGGTGTGAGTGGGCTGATTTGCCCTATGAGATGATTTATGGAGATGCCCTTCG 900  
DB 869 GTGACTGTGGTGTGAGTGGGCTGATTTGCCCTATGAGATGATTTATGGAGATGCCCTTCG 928  
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QY 1021 GCCAGAAAGAGAGACTGAAAGTTTGAAGGTCTTTGTGCCATCTTTCTCTTAAATTTG 1080  
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; Sequence 51. Application PC/TUS0400750
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
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; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007
; CURRENT APPLICATION NUMBER: PCT/US04/00750
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)...(6180)
PCT-US04-00750-51

Query Match      93.1%; Score 1381.8; DB 2; Length 6574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1386; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY      61 CTTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACACCTTTATGATCTCAACAGCAGATGT 120
Db      89 CTTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACACCTTTATGATCTCAACAGCAGATGT 148
QY      121 CTCTCTTTCCAGAGAGGATATTAGATGCCCTCTTTGTTCTTTGAGATGAGTC 180
Db      149 CTCTCTTTCCAGAGAGGATATTAGATGCCCTCTTTGTTCTTTGAGATGAGTC 208
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Qy	1381	AGTGTCAAAAGT	1393
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Perfect score: 1481

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Gapop 10\_0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1476.2	99.7	2066	17	US-10-311-034-33
5	1388.2	93.7	1870	17	US-10-262-511-3
6	1388.2	93.7	5877	13	US-10-028-946-3
7	1388.2	93.7	5877	18	US-10-791-666-3
8	1388.2	93.7	6165	13	US-10-028-946-1
9	1388.2	93.7	6165	18	US-10-791-666-1
10	1388.2	93.7	6298	17	US-10-415-011-43
11	1381.8	93.3	6159	13	US-10-017-216-3
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14	1381.8	93.3	6574	16	US-10-325-430-10	Sequence 10, Appli
15	1381.8	93.3	6574	18	US-10-757-262-51	Sequence 51, Appli
16	1372	92.6	8556	18	US-10-618-941-1	Sequence 1, Appli
17	1365.8	92.2	6189	11	US-09-964-956-10	Sequence 10, Appli
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19	1365.8	92.2	6201	11	US-09-964-956-8	Sequence 8, Appli
20	1365.8	92.2	6201	17	US-10-262-511-13	Sequence 13, Appli
21	947.2	64.0	2162	17	US-10-120-988-419	Sequence 419, App
22	945.4	63.8	957	17	US-10-412-897-1	Sequence 1, Appli
23	744.8	50.3	1333	14	US-10-282-048-1	Sequence 1, Appli
24	578.8	39.1	2896	18	US-10-357-930-30150	Sequence 30150, A
25	441.8	29.8	446	18	US-10-357-930-15814	Sequence 15814, A
26	434.4	29.3	485	18	US-10-357-930-45643	Sequence 45643, A
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31	246.8	16.7	5438	18	US-10-618-941-2	Sequence 2, Appli
32	240	16.2	6335	17	US-10-388-934-85	Sequence 85, Appli
33	238.8	16.1	5373	18	US-10-702-496-5	Sequence 5, Appli
34	236.8	16.0	4917	18	US-10-385-163-121	Sequence 121, App
35	236.8	16.0	4917	18	US-10-796-177-121	Sequence 121, App
36	234.6	15.8	2785	17	US-10-172-118-930	Sequence 930, App
37	234.6	15.8	2785	17	US-10-342-887-930	Sequence 930, App
38	234.6	15.8	2785	19	US-10-848-755A-116	Sequence 116, App
39	234.6	15.8	5694	17	US-10-288-798-26	Sequence 26, Appli
40	234.6	15.8	5694	17	US-10-362-892-26	Sequence 26, Appli
41	234.6	15.8	7151	17	US-10-433-794-39	Sequence 39, Appli
42	231.4	15.6	2621	16	US-10-252-157-179	Sequence 179, App
43	228	15.4	5347	17	US-10-210-130-99	Sequence 99, Appli
44	228	15.4	5875	17	US-10-210-130-101	Sequence 101, App
45	225.6	15.2	3407	9	US-09-971-845-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-804-471A-1  
; Sequence 1, Application US/09804471A  
; Patent No. US2002013222A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; THEREOF  
; FILE REFERENCE: CL001164  
; CURRENT APPLICATION NUMBER: US/09/804,471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Human  
US-09-804-471A-1

Query Match 100.0%; Score 1481; DB 9; Length 1515;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 1481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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Qy	121	CTCCTCTTCCGAGAGGATATTAGATGCCCTCTTCTTCTTGAAGATGCAGTC	180		

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Db 197 AGCTGCTCTGATGAAGATTAAAGCAGTGAGCAACTTTGTCGGAAGTATTCCGACACCA 256  
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Qy 301 GTTGTGCTCACTTTGCTGAAGTCAGGTGATGAAGAGCAACCCGGGACATCTATG 360  
Db 317 GTTGTGCTCACTTTGCTGAAGTCAGGTGATGAAGAGCAACCCGGGACATCTATG 376  
Qy 361 CTATGAAGTCAGAGAGAGGCTTTATTTGGCCAGGAGAGGTTTCAATTTTGTAGG 420  
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Qy 481 TTCAGGACAAAATCACCTTTATCTGTCATGGAATATCAGCTCGAGGGGACTTGTCTG 540  
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## RESULT 2

US-10-238-709-1  
; Sequence 1, Application US/10238709  
; Publication No. US20030022340A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; CURRENT FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
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; ORGANISM: Human  
US-10-238-709-1

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 797 TGGCTCCTGAAGTCTGACTGTGATGAACGGGATGAAAGGACCTACGCGCTGACT 856  
 Db |||||  
 Qy 841 GTGACTGGTGTGAGTGGGCTGATGCTCTATGAGATGATTTATGGAGATCCCGCTTCG 900  
 Db GTGACTGGTGTGAGTGGGCTGATGCTCTATGAGATGATTTATGGAGATCCCGCTTCG 916  
 Qy 901 CAGAGGAACCTCTGCCAGAACCTTCAATTAATATGAATTTCCAGGGTTTTTGAAT 960  
 Db CAGAGGAACCTCTGCCAGAACCTTCAATTAATATGAATTTCCAGGGTTTTTGAAT 976  
 Qy 961 TTCCAGATGACCCCAAGTGAAGTCTCTTCTGATCTGATTCAGGCTTGTGGCG 1020  
 Db TTCCAGATGACCCCAAGTGAAGTCTCTTCTGATCTGATTCAGGCTTGTGGCG 1036  
 Qy 1021 GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTCTGCTGCCATCTTCTCTCTAAATTTG 1080  
 Db GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTCTGCTGCCATCTTCTCTCTAAATTTG 1096  
 Qy 1081 ACTGGAACACATTCGTAACTCTCTCCCGCTTGGTTCGACCTCAAGTCGACATG 1140  
 Db ACTGGAACACATTCGTAACTCTCTCCCGCTTGGTTCGACCTCAAGTCGACATG 1156  
 Qy 1141 ACACCTCAATTTTGAATGAACACAGAGAAGTTCGTCGGTTCATCTCTCCGTGCCAGC 1200  
 Db ACACCTCAATTTTGAATGAACACAGAGAAGTTCGTCGGTTCATCTCTCCGTGCCAGC 1216  
 Qy 1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGGGGTTTTTGTACAGCAAG 1260  
 Db TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGGGGTTTTTGTACAGCAAG 1276  
 Qy 1261 CACTGGGATCTTGGTAGATCTGAGTCTGTGTGTCGGTCTGGACTCCCTGCCAAGA 1320  
 Db CACTGGGATCTTGGTAGATCTGAGTCTGTGTGTCGGTCTGGACTCCCTGCCAAGA 1336  
 Qy 1321 CTAGCTCCATGGAAGAACTCTCATCAAAAGCAAGAGCTACAAGCTCTCAGGACA 1380  
 Db CTAGCTCCATGGAAGAACTCTCATCAAAAGCAAGAGCTACAAGCTCTCAGGACA 1396  
 Qy 1381 AGTGTCAGAGTATTTATTTCCGACCGCGCTCTCTTCTCTGCTCCAGGATCCTCCGT 1440  
 Db AGTGTCAGAGTATTTATTTCCGACCGCGCTCTCTTCTCTGCTCCAGGATCCTCCGT 1456  
 Qy 1441 CCGTATATGCCAGGATCGCCCGGCGGCTGCTGGCTC 1481  
 Db CCGTATATGCCAGGATCGCCCGGCGGCTGCTGGCTC 1497

RESULT 4

US-10-311-034-33  
 ; Sequence 33, Application US/10311034  
 ; Publication No. US20040023242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.  
 ; APPLICANT: YUE, Henry  
 ; APPLICANT: LAL, Preeti  
 ; APPLICANT: BANDMAN, Olga  
 ; APPLICANT: BOROWSKI, Mark L.  
 ; APPLICANT: AU-YOUNG, Janice  
 ; APPLICANT: LU, Yan  
 ; APPLICANT: GANDHI, Ameena R.  
 ; APPLICANT: TRIBOULEY, Catherine M.  
 ; APPLICANT: CHAWLA, Narinder K.  
 ; APPLICANT: YAO, Monique G.  
 ; APPLICANT: LU, Dyung Aina M.  
 ; APPLICANT: GREENWALD, Sara R.  
 ; APPLICANT: RAMKUNAR, Javalaxmi  
 ; APPLICANT: GRIFFIN, Jennifer A.  
 ; APPLICANT: KEARNEY, Liam  
 ; APPLICANT: BURFORD, Neil  
 ; APPLICANT: NGUYEN, Daniel B.  
 ; APPLICANT: TANG, Y. Tom

; APPLICANT: BAUGHN, Mariah R.  
 ; APPLICANT: HE, Ann  
 ; APPLICANT: THORNTON, Michael  
 ; APPLICANT: HAFALIA, April  
 ; APPLICANT: ARVIZU, Chandra S.  
 ; APPLICANT: GURURAJAN, Rajagopal  
 ; APPLICANT: LO, Terence P.  
 ; APPLICANT: KHAH, Farrah A.  
 ; APPLICANT: RECIPON, Shirley A.  
 ; APPLICANT: AZIMZAI, Yalda  
 ; APPLICANT: POLICKY, Jennifer L.  
 ; APPLICANT: DING, Li  
 ; APPLICANT: GREYER, Megan  
 ; APPLICANT: ELLIOTT, Vicki S.  
 ; APPLICANT: THANGAVELU, Kavitha  
 ; APPLICANT: BATRA, Sajeev  
 ; APPLICANT: ISON, Craig H.  
 ; TITLE OF INVENTION: HUMAN KINASES  
 ; FILE REFERENCE: PI-0125 PCT  
 ; CURRENT APPLICATION NUMBER: US/10/311,034  
 ; CURRENT FILING DATE: 2002-12-10  
 ; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
 ; 60/228,056  
 ; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 33  
 ; LENGTH: 2066  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CB1  
 ; US-10-311-034-33

Query Match 99.7%; Score 1476.2; DB 17; Length 2066;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1478; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 TCAATATGAGCGCGGAATCCTTTGGATGCTGGTGTGCTGTGCTGAACCCATTGCCAACCGGG 60  
 Db 24 TCAATATGAGCGCGGAATCCTTTGGATGCTGGTGTGCTGTGCTGAACCCATTGCCAACCGGG 83  
 Qy 61 CTCTCAGGCTGAATCTGTTCTCCAGGGAAACCACTTTATGACTCAACAGAGATGT 120  
 Db 84 CTCTCAGGCTGAATCTGTTCTCCAGGGAAACCACTTTATGACTCAACAGAGATGT 143  
 Qy 121 CTCTCTTTCCCGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGATGCAGTC 180  
 Db 144 CTCTCTTTCCCGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGATGCAGTC 203  
 Qy 181 AGCTCTCTGTATGAAGATTAAGACGTGAGCAACTTTGTCCGAAAGTATTCGACACCA 240  
 Db 204 AGCTCTCTGTATGAAGATTAAGACGTGAGCAACTTTGTCCGAAAGTATTCGACACCA 263  
 Qy 241 TAGCTGAGTTACAGGAGCTCCAGCTTCGCAAGAGCACTTCGAAGTCTGAGTCTGTAG 300  
 Db 264 TAGCTGAGTTACAGGAGCTCCAGCTTCGCAAGAGCACTTCGAAGTCTGAGTCTGTAG 323  
 Qy 301 GTGTGCTCCTTTGCTGAAGTGCAGTGGTGAAGAGAAAGCAACCGGGGACATCTATG 360  
 Db 324 GTGTGCTCCTTTGCTGAAGTGCAGTGGTGAAGAGAAAGCAACCGGGGACATCTATG 383  
 Qy 361 CTATGAAGTGAAGAGAGGCTTTATTTGGCCCGAGGAGAGGTTTCAATTTTGGAG 420  
 Db 384 CTATGAAGTGAAGAGAGGCTTTATTTGGCCCGAGGAGAGGTTTCAATTTTGGAG 443  
 Qy 421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGGTGATCCCGCAATTACAGTATGCCT 480  
 Db 444 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGGTGATCCCGCAATTACAGTATGCCT 503  
 Qy 481 TTCAGGACAAAATCACTTTTATCTGGTCAATGGAATATCAGCCTGGAGGGGACTTGTGT 540







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QY 421 AAGAGCGGAACATATTATCTCGAAGACCAAGCCCGTGGATCCCCCAATTTACAGTATGCCT 480
DB 431 AAGAGCGGAACATATTATCTCGAAGACCAAGCCCGTGGATCCCCCAATTTACAGTATGCCT 490
QY 481 TTCAGAGCAAAATACACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTCTGT 540
DB 491 TTCAGAGCAAAATACACCTTTATCTGGTCATGGAATATCAGCCTGAGGGGACTTCTGT 550
QY 541 CACTTTTGAATAGATATGAGGACCACTAGATCAAAACCTGTATACACAGTTTACCTAGCTG 600
DB 551 CACTTTTGAATAGATATGAGGACCACTAGATCAAAACCTGTATACACAGTTTACCTAGCTG 610
QY 601 AGCTGATTTTGGCTGTTTCAGCGTTTCATCTGATGGGATACGTGCAATCAGACATCAAGC 660
DB 611 AGCTGATTTTGGCTGTTTCAGCGTTTCATCTGATGGGATACGTGCAATCAGACATCAAGC 670
QY 661 CTGAGAACATTTCTGGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
DB 671 CTGAGAACATTTCTGGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730
QY 721 CGAAATGAAATTCAAACAGATGCTGAATGCCAAACTCCCGATTGGGACCCACAGATTACA 780
DB 731 CGAAATGAAATTCAAACAGATGCTGAATGCCAAACTCCCGATTGGGACCCACAGATTACA 790
QY 781 TGGCTCCTGAAAGTGTGACTGTGATGAACGGGGATGGAAGGACCTACGGCCTGGACT 840
DB 791 TGGCTCCTGAAAGTGTGACTGTGATGAACGGGGATGGAAGGACCTACGGCCTGGACT 850
QY 841 GTGACTGGTGGTCAAGTGGGCGTGAATGCTTATGAGATGATTTATGGAGATCCCTCTCG 900
DB 851 GTGACTGGTGGTCAAGTGGGCGTGAATGCTTATGAGATGATTTATGGAGATCCCTCTCG 910
QY 901 CAGAGGAACTCTGCCAGAACCTTCAATAACATTATGAATTCACAGCGTTTTTCAAAAT 960
DB 911 CAGAGGAACTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGTTTTTCAAAAT 970
QY 961 TTCAGATGACCCCAAGTGAGCAGTGACTTTCTTGATCTGATTTCAAAAGCTTGTGTGGG 1020
DB 971 TTCAGATGACCCCAAGTGAGCAGTGACTTTCTTGATCTGATTTCAAAAGCTTGTGTGGG 1030
QY 1021 GCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGGCAATCTTTCTCTTAAATTTG 1080
DB 1031 GCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGGCAATCTTTCTCTTAAATTTG 1090
QY 1081 ACTGGAAACATTTCTGCTCTCTCCCTTCTGTTCCACCTCAAGTCCGAGATG 1140
DB 1091 ACTGGAAACATTTCTGCTCTCTCCCTTCTGTTCCACCTCAAGTCTGAGATG 1150
QY 1141 ACACCTCCCAATTTTGATGAACAGAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1200
DB 1151 ACACCTCCCAATTTTGATGAACAGAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1210
QY 1201 TGAGCCCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGGTTTTTGTACAGCAAGG 1260
DB 1211 TGAGCCCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGGTTTTTGTACAGCAAGG 1270
QY 1261 CACTGGGGATTTCTGGTGAATCTGAGTCTGTTGTGTGGGTTCTGGACTCCCTGCCAAG 1320
DB 1271 CACTGGGGATTTCTGGTGAATCTGAGTCTGTTGTGTGGGTTCTGGACTCCCTGCCAAG 1330
QY 1321 CTAGCTCCATGGAAAGAAACTTCTCATCAAAAGCAAGAGCTTCAAGACTCTCAGGACA 1380
DB 1331 CTAGCTCCATGGAAAGAAACTTCTCATCAAAAGCAAGAGCTTCAAGACTCTCAGGACA 1390
QY 1381 AGTGTCAAGGT 1393
DB 1391 AGTGTCAAGAT 1403
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RESULT 7

US-10-791-666-3

; Sequence 3, Application US/10791666

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; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fridele, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-791-666-3
```

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Query Match 93.7%; Score 1388.2; DB 18; Length 5877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 TCAAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAACCCATTTGCCAACCGGG 60
DB 11 TCAAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAACCCATTTGCCAACCGGG 70
QY 61 CTCTCAGGCTGAATCTGTCTTCCAGGGGAAACACCCCTTTATGACTCAACAGCAGATGT 120
DB 71 CTCTCAGGCTGAATCTGTCTTCCAGGGGAAACACCCCTTTATGACTCAACAGCAGATGT 130
QY 121 CTCTCTTTCCCGAGAAGGATATAGATGCCCTCTTTGCTCTCTTTGAAGAAATGCAGTC 180
DB 131 CTCTCTTTCCCGAGAAGGATATAGATGCCCTCTTTGCTCTCTTTGAAGAAATGCAGTC 190
QY 181 AGCCTGCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTTCCGGAAGTATTCGACACCA 240
DB 191 AGCCTGCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTTCCGGAAGTATTCGACACCA 250
QY 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAACTCAGAACTCTGTAG 300
DB 251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAACTCAGAACTCTGTAG 310
QY 301 GTTGTGCTCAGCTTTCGCTGAAGTGCAAGTGTAGAGAGAAAGCAACCGGGGACATCTATG 360
DB 311 GTTGTGCTCAGCTTTCGCTGAAGTGCAAGTGTAGAGAGAAAGCAACCGGGGACATCTATG 370
QY 361 CTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCCGAGGAGGTTTCAATTTTTTGGAG 420
DB 371 CTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCCGAGGAGGTTTCAATTTTTTGGAG 430
QY 421 AAGAGCGGAACATATTATCTCGAAGACCAAGCCCGTGGATCCCCCAATTTACAGTATGCCT 480
DB 431 AAGAGCGGAACATATTATCTCGAAGACCAAGCCCGTGGATCCCCCAATTTACAGTATGCCT 490
QY 481 TTCAGAGCAAAATACACCTTTATCTGGTCAATGGAATATCAGCCTGAGGGGACTTCTGT 540
DB 491 TTCAGAGCAAAATACACCTTTATCTGGTCAATGGAATATCAGCCTGAGGGGACTTCTGT 550
QY 541 CACTTTTGAATAGATATGAGGACCACTAGATGAAACCTGTATACAGTTTACCTAGCTG 600
DB 551 CACTTTTGAATAGATATGAGGACCACTAGATGAAACCTGTATACAGTTTACCTAGCTG 610
QY 601 AGCTGATTTTGGCTGTTTCAGCGTTTCATCTGATGGGATACGTGCAATCAGACATCAAGC 660
DB 611 AGCTGATTTTGGCTGTTTCAGCGTTTCATCTGATGGGATACGTGCAATCAGACATCAAGC 670
QY 661 CTGAGAACATTTCTGGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
DB 671 CTGAGAACATTTCTGGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730
```



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QY 1081 ACTGGAACAACATTGTAACCTCTCTCCCTCCCTCTCGTTCCACCCCTCAAGTCCGAGCATG 1140
DB 1091 ACTGGAACAACATTGTAACCTCTCTCCCTCCCTCTCGTTCCACCCCTCAAGTCTGACGATG 1150
QY 1141 ACACCTCCCAATTTGTATGAACACGAGAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1200
DB 1151 ACACCTCCCAATTTGTATGAACACGAGAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1210
QY 1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGG 1260
DB 1211 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGG 1270
QY 1261 CACTGGGATTTCTTGGTAGATCTGAGTCTGTGTGTGGGTCTGGACTCCCTGCCAAGA 1320
DB 1271 CACTGGGATTTCTTGGTAGATCTGAGTCTGTGTGTGGGTCTGGACTCCCTGCCAAGA 1330
QY 1321 CTAGCTCCATGGAAGAAATCTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1380
DB 1331 CTAGCTCCATGGAAGAAATCTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1390
QY 1381 AGTGTCAAGGT 1393
DB 1391 AGTGTCAAGAT 1403
```

## RESULT 9

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US-10-791-666-1
; Sequence 1, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; PRIOR FILING DATE: 2004-03-02
; PRIOR FILING DATE: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-791-666-1
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Query Match 93.7%; Score 1388.2; DB 18; Length 6165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCAATATGAGCGCGGAATCCCTTTGGATGCTGGTGTGCTGAACCCATTCGCAACCGGG 60
DB 11 TCAATATGAGCGCGGAATCCCTTTGGATGCTGGTGTGCTGAACCCATTCGCAACCGGG 70
QY 61 CTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCCCTTATGACTCAACAGCAGATGT 120
DB 71 CTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCCCTTATGACTCAACAGCAGATGT 130
QY 121 CTCCTCTTCCGAGAGGATATTAGTGCCTCTTGTCTCTTTGGATGAGTGCAGTC 180
DB 131 CTCCTCTTCCGAGAGGATATTAGTGCCTCTTGTCTCTTTGGATGAGTGCAGTC 190
QY 181 AGCTGCTCTGATGAAGATTAAAGCAGTGAACAACTTGTCCGGAAGTATTCCGACACCA 240
DB 191 AGCTGCTCTGATGAAGATTAAAGCAGTGAACAACTTGTCCGGAAGTATTCCGACACCA 250
QY 241 TAGCTCAGTTACAGGAGCTCCAGCTTCGCGCAAGAGCTTCGAAGTCAAGATCTTGTAG 300
DB 251 TAGCTCAGTTACAGGAGCTCCAGCTTCGCGCAAGAGCTTCGAAGTCAAGATCTTGTAG 310
```

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QY 301 GTTGTGTCACATTGCTGAAGTGCAGTGGTAAGAGAGAAAGCAACCGGGAACATCTATG 360
DB 311 GTTGTGTCACATTGCTGAAGTGCAGTGGTAAGAGAGAAAGCAACCGGGAACATCTATG 370
QY 361 CTATGAAAGTGAATGAAGAAAGGCTTTATTTGSCCCAGAGAGAGGTTTCAATTTTGTAGG 420
DB 371 CTATGAAAGTGAATGAAGAAAGGCTTTATTTGSCCCAGAGAGAGGTTTCAATTTTGTAGG 430
QY 421 AAGAGCGGAACATATTTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTTACAGTATGCT 480
DB 431 AAGAGCGGAACATATTTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTTACAGTATGCT 490
QY 481 TTCAAGACAAAAATCACTTTTATCTGGTCAATGGAATATCAGCCTGGAGGGGACTTGTCTG 540
DB 491 TTCAAGACAAAAATCACTTTTATCTGGTCAATGGAATATCAGCCTGGAGGGGACTTGTCTG 550
QY 541 CACTTTTGAATAGATAGAGACCAAGTATAGATGAAGAAACCTGTATACAGTTTACCTAGCTG 600
DB 551 CACTTTTGAATAGATAGAGACCAAGTATAGATGAAGAAACCTGTATACAGTTTACCTAGCTG 610
QY 601 AGCTGATTTTGGCTGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAG 660
DB 611 AGCTGATTTTGGCTGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAG 670
QY 661 CTGAGAAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720
DB 671 CTGAGAAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730
QY 721 CGAAAAATGAATTCAAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCAGATTTACA 780
DB 731 CGAAAAATGAATTCAAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCAGATTTACA 790
QY 781 TGGCTCTCAAGTGTGACTGTGATGAACCGGGATGGAAAGGCACTACGGGCTGGACT 840
DB 791 TGGCTCTCAAGTGTGACTGTGATGAACCGGGATGGAAAGGCACTACGGGCTGGACT 850
QY 841 GTGACTGGTGGTCAAGTGGGCTGATTCCTATGAGATGATTTATGGAGATCCCCCTTCG 900
DB 851 GTGACTGGTGGTCAAGTGGGCTGATTCCTATGAGATGATTTATGGAGATCCCCCTTCG 910
QY 901 CAGAGGAAACCTCTGCCAGAACTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAT 960
DB 911 CAGAGGAAACCTCTGCCAGAACTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAT 970
QY 961 TTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
DB 971 TTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1030
QY 1021 GCCAGAAAGAGAGACTGAAAGTTTGAAGTCTTTGCTGCCATCTTTCTCTTAAATTTG 1080
DB 1031 GCCAGAAAGAGAGACTGAAAGTTTGAAGTCTTTGCTGCCATCTTTCTCTTAAATTTG 1090
QY 1081 ACTGGAACAACTTGTAACTCTCTCTCCCTCTGTTCCCACTCAAGTCCGAGATG 1140
DB 1091 ACTGGAACAACTTGTAACTCTCTCTCCCTCTGTTCCCACTCAAGTCTGAGATG 1150
QY 1141 ACACCTCCCAATTTGTATGAACCAAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1200
DB 1151 ACACCTCCCAATTTGTATGAACCAAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1210
QY 1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGG 1260
DB 1211 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCGTACAGCAAGG 1270
QY 1261 CACTGGGATTTCTTGGTAGATCTGAGTCTGTGTGTGGGTCTGGACTCCCTGCCAAGA 1320
DB 1271 CACTGGGATTTCTTGGTAGATCTGAGTCTGTGTGTGGGTCTGGACTCCCTGCCAAGA 1330
QY 1321 CTAGCTCCATGGAAGAAATCTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1380
DB 1331 CTAGCTCCATGGAAGAAATCTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA 1390
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Qy 1381 AGTGTCAAGGT 1393
Db 1391 AGTGTCAAGAT 1403

RESULT 10
US-10-415-011-43
; Sequence 43, Application US/10415011
; Publication No. US20040053394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAPALIA, April J.A.
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: BOROWSKI, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER, Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCES: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/47728
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 43
; LENGTH: 6298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CB1
US-10-415-011-43

Query Match 93.7%; Score 1388.2; DB 17; Length 6298;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1145 ACTGGAACACATTCGTAACCTCTCTCCCTCCCTTCGTTCCACCTCAAGTCTGAGCATG 1204  
QY 1141 ACACCTCCCAATTTTGATGACACAGAGAAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200  
Db 1205 ACACCTCCCAATTTTGATGACACAGAGAAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1264  
QY 1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTCGTACAGCAAGG 1260  
Db 1265 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTCGTACAGCAAGG 1324  
QY 1261 CACTGGGATTTCTGTGATGATCTGATCTGTTGTGTCGGGTTCGACTCCCTGCCAAGA 1320  
Db 1325 CACTGGGATTTCTGTGATGATCTGATCTGTTGTGTCGGGTTCGACTCCCTGCCAAGA 1384  
QY 1321 CTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTACAGACTCTCAGGACA 1380  
Db 1385 CTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTACAGACTCTCAGGACA 1444  
QY 1381 AGTGTCACAAGGT 1393  
Db 1445 AGTGTCACAAGAT 1457

## RESULT 11

US-10-017-216-3  
; Sequence 3, Application US/10017216  
; Publication No. US20020160483A1  
; GENERAL INFORMATION:  
; APPLICANT: KAPPELER-LIBERMANN, Rosana  
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prob  
; TITLE OF INVENTION: Kinase and Uses Therefor  
; FILE REFERENCE: 10147-57U1  
; CURRENT APPLICATION NUMBER: US/10/017,216  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 6159  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-017-216-3

Query Match 93.3%; Score 1381.8; DB 13; Length 6159;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1386; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 TCAATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATTTGCCAACCGGG 60  
Db 11 TCNATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATTTGCCAACCGGG 70  
QY 61 CTTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATGACTCAACAGCAGATGT 120  
Db 71 CTTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATGACTCAACAGCAGATGT 130  
QY 121 CTCCTCTTCCGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGATGAGTC 180  
Db 131 CTCCTCTTCCGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGATGAGTC 190  
QY 181 AGCTCTCTGTGAAGATTAAAGCAGTGAACAACTTTGTCGGAAGATTTCGACACCA 240  
Db 191 AGCTCTCTGTGAAGATTAAAGCAGTGAACAACTTTGTCGGAAGATTTCGACACCA 250  
QY 241 TAGCTGAGTTACAGGAGCTCCAGCTTCCGCAAGGACTTTGGAAGTCAAGAGTCTTTAG 300  
Db 251 TAGCTGAGTTACAGGAGCTCCAGCTTCCGCAAGGACTTTGGAAGTCAAGAGTCTTTAG 310  
QY 301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGTTAGAGAGAAAGCAACCGGGGACATCTATG 360  
Db 311 GTTGTGGTCACTTTGCTGAAGTGCAGGTGTTAGAGAGAAAGCAACCGGGGACATCTATG 370

QY 361 CTATGAAAGTGTATGAAGAAAGAGGCTTTATTTGGCCAGAGCAGGTTTCATTTTTTGGAG 420  
Db 371 CTATGAAAGTGTATGAAGAAAGAGGCTTTATTTGGCCAGAGCAGGTTTCATTTTTTGGAG 430  
QY 421 AAGAGCGGAACATATTTATCTCGAAGCAAAAGCCCGTGGATCCCCCAATTTACAGTATGCCT 480  
Db 431 AAGAGCGGAACATATTTATCTCGAAGCAAAAGCCCGTGGATCCCCCAATTTACAGTATGCCT 490  
QY 481 TTCAAGGACAAAATACACCTTTTATCTGGTCAATGGAATATCAGCCCTGAGGGGACTTGTCTGT 540  
Db 491 TTCAAGGACAAAATACACCTTTTATCTGGTCAATGGAATATCAGCCCTGAGGGGACTTGTCTGT 550  
QY 541 CACTTTTGAATAGATATGAGGACCAAGTTAGATGAAAACCTGTATACAGTATTTACCTAGCTG 600  
Db 551 CACTTTTGAATAGATATGAGGACCAAGTTAGATGAAAACCTGTATACAGTATTTACCTAGCTG 610  
QY 601 AGCTGATTTTGGCTGTTTACAGGCTTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660  
Db 611 AGCTGATTTTGGCTGTTTACAGGCTTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670  
QY 661 CTGAGAAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCGG 720  
Db 671 CTGAGAAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCGG 730  
QY 721 CGAAAATGAATTCAAAACAGATGGTGAATGCCAAACTCCCGATTTGGGACCCACAGATTACA 780  
Db 731 CGAAAATGAATTCAAAACAGATGGTGAATGCCAAACTCCCGATTTGGGACCCACAGATTACA 790  
QY 781 TGGCTCTCAAGTGTGACTGTGATGAACGGGGATGAAAAGCACCTACGGCTGGACT 840  
Db 791 TGGCTCTCAAGTGTGACTGTGATGAACGGGGATGAAAAGCACCTACGGCTGGACT 850  
QY 841 GTGACTGGTGGTCAAGTGGGCGTGAATTCCTATGAGATGATTTATGGAGATCCCTCTTCG 900  
Db 851 GTGACTGGTGGTCAAGTGGGCGTGAATTCCTATGAGATGATTTATGGAGATCCCTCTTCG 910  
QY 901 CAGAGGAAACCTCTGCCAGAACCTTCAATAACATATTAATTTCCAGCGTTTTTGAAT 960  
Db 911 CAGAGGAAACCTCTGCCAGAACCTTCAATAACATATTAATTTCCAGCGTTTTTGAAT 970  
QY 961 TTCCAGATGACCCCAAGTGGAGCAGTGAATTTCTGATCTGATTTCAAGCTTTGTGGCG 1020  
Db 971 TTCCAGATGACCCCAAGTGGAGCAGTGAATTTCTGATCTGATTTCAAGCTTTGTGGCG 1030  
QY 1021 GCCAGAAACAGAGACTGAAAGTTTGAAGTCTTTGCTGCCATCCTTTCTCTTAAATTCG 1080  
Db 1031 GCCAGAAACAGAGACTGAAAGTTTGAAGTCTTTGCTGCCATCCTTTCTCTTAAATTCG 1090  
QY 1081 ACTGGAACAACTTCGTAACTCTCTCCCTCCCTTTCGTTCCACCTCAAGTCCGAGCATG 1140  
Db 1091 ACTGGAACAACTTCGTAACTCTCTCCCTCCCTTTCGTTCCACCTCAAGTCCGAGCATG 1150  
QY 1141 ACACCTTCAATTTTGAATGAACAGAGAAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200  
Db 1151 ACACCTTCAATTTTGAATGAACAGAGAAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1210  
QY 1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTCGTACAGCAAGG 1260  
Db 1211 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTCGTACAGCAAGG 1270  
QY 1261 CACTGGGATTTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCTGCCAAGA 1320  
Db 1271 CACTGGGATTTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCTGCCAAGA 1330  
QY 1321 CTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTTCAAGACTCTCAGGACA 1380  
Db 1331 CTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTTCAAGACTCTCAGGACA 1390  
QY 1381 AGTGTCACAAGGT 1393  
Db 1391 AGTGTCACAAGAT 1403

RESULT 12

US-10-325-430-11  
; Sequence 11, Application US/10325430  
; Publication No. US20030153525A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Rosenfeld, Julie Beth  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,  
; FILE REFERENCE: MP101-294PIRNM  
; CURRENT APPLICATION NUMBER: US/10/325,430  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/341,953  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 6162  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(6162)  
US-10-325-430-11

Query Match 93.3%; Score 1381.8; DB 16; Length 6162;

Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1386; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY	1	TCAAATATGAGCGCGGAATCTTTGGATCGTGTGCTGCTGAACCCATTGCCAACCGGG	60
DB	11	TCAAATATGAGCGCGGAATCTTTGGATCGTGTGCTGCTGAACCCATTGCCAACCGGG	70
QY	61	CTCCAGGCTGAATCTCTTCTCCAGGGGAACACCCCTTTATGACTCAACAGCAGATGT	120
DB	71	CTCCAGGCTGAATCTCTTCTCCAGGGGAACACCCCTTTATGACTCAACAGCAGATGT	130
QY	121	CTCCTCTTCCGAGAGGATATAGATGCCCTCTTGTCTCTTTGAAGATGCAATC	180
DB	131	CTCCTCTTCCGAGAGGATATAGATGCCCTCTTGTCTCTTTGAAGATGCAATC	190
QY	181	AGCTGCTCTGATGAAGATTAAGCAGTGAACAACTTTGCGGAAGTATTCGACACCA	240
DB	191	AGCTGCTCTGATGAAGATTAAGCAGTGAACAACTTTGCGGAAGTATTCGACACCA	250
QY	241	TAGCTGATTTACAGGAGCTCCAGCCTTCGGAAGGACTTCGAAGTCAGAACTTTGTAG	300
DB	251	TAGCTGATTTACAGGAGCTCCAGCCTTCGGAAGGACTTCGAAGTCAGAACTTTGTAG	310
QY	301	GTGTGTGCTCACTTGTGTAAGTGCAGTGTGTAAGAGAGAAAGCAACCGGGGACATCATG	360
DB	311	GTGTGTGCTCACTTGTGTAAGTGCAGTGTGTAAGAGAGAAAGCAACCGGGGACATCATG	370
QY	361	CTATGAAGTGTGAAGAGAGCTTTATTTGGCCAGGAGCAGGTTTCAATTTTGTAGG	420
DB	371	CTATGAAGTGTGAAGAGAGCTTTATTTGGCCAGGAGCAGGTTTCAATTTTGTAGG	430
QY	421	AAGAGCGGAACATATTATTCGAAGCAACAAGCCGCTGGATCCGCCAATTAACAGTATGCCT	480
DB	431	AAGAGCGGAACATATTATTCGAAGCAACAAGCCGCTGGATCCGCCAATTAACAGTATGCCT	490
QY	481	TTGAGGCAAAATACCTTTATCTGTCATGAATATCAGCTCGGAGGAGCTTCTGT	540
DB	491	TTGAGGCAAAATACCTTTATCTGTCATGAATATCAGCTCGGAGGAGCTTCTGT	550
QY	541	CACCTTTGAATAGATAGAGACCAAGTATGATGAACCTGATACAGTATTTACCTAGCTG	600
DB	551	CACCTTTGAATAGATAGAGACCAAGTATGATGAACCTGATACAGTATTTACCTAGCTG	610
QY	601	AGCTGATTTTGGCTGTTTCAGCGGTTCACTCTGATGGGATACGTGTCATCGAGACATCAAGC	660

DB	611	AGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGATACGTGTCATCGAGACATCAAGC	670
QY	661	CTGAGAAACATTTCTGTTGACCGGCACAGGACACATCAAGCTGTGGATTTTGGATCTGCCG	720
DB	671	CTGAGAAACATTTCTGTTGACCGGCACAGGACACATCAAGCTGTGGATTTTGGATCTGCCG	730
QY	721	CGAAAAATGAATTCAAAACAAGATGGTGAATGCCAAATCCCGATTGGGACCCAGATTACA	780
DB	731	CGAAAAATGAATTCAAAACAAGATGGTGAATGCCAAATCCCGATTGGGACCCAGATTACA	790
QY	781	TGCTCTCTGAAGTGTGCTGCTGATGAACGGGGATGAAAAGGCACCTACGGCTGGAAT	840
DB	791	TGCTCTCTGAAGTGTGCTGCTGATGAACGGGGATGAAAAGGCACCTACGGCTGGAAT	850
QY	841	GTGACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
DB	851	GTGACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	910
QY	901	CAGAGGGAACCTCTGCGCAGAACCTTCAATAACATTAATTAATTTCCAGCGGTTTTCGAAT	960
DB	911	CAGAGGGAACCTCTGCGCAGAACCTTCAATAACATTAATTAATTTCCAGCGGTTTTCGAAT	970
QY	961	TTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1020
DB	971	TTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1030
QY	1021	GCCAGAAAGAGAGACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	1080
DB	1031	GCCAGAAAGAGAGACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	1090
QY	1081	ACTGGAACCAACATTCCTTAACCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	1140
DB	1091	ACTGGAACCAACATTCCTTAACCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	1150
QY	1141	ACACCTCCAAATTTGATGAACAGAGAAATTCGTTGGTTCATCTCTCCGTCGACG	1200
DB	1151	ACACCTCCAAATTTGATGAACAGAGAAATTCGTTGGTTCATCTCTCCGTCGACG	1210
QY	1201	TGAGCCCTCAGCTTCTCGGGTGAAGAACTGCGGTTTGGGGTTTTCGTACAGCAAG	1260
DB	1211	TGAGCCCTCAGCTTCTCGGGTGAAGAACTGCGGTTTGGGGTTTTCGTACAGCAAG	1270
QY	1261	CAGTGGGATTTCTTGTGTAGATCTGAGTCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGT	1320
DB	1271	CAGTGGGATTTCTTGTGTAGATCTGAGTCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGT	1330
QY	1321	CTAGCTCCATGGAAGAAACCTTCTCATCAAAAGCAAGAGCTACAGACTCTCAGGACA	1380
DB	1331	CTAGCTCCATGGAAGAAACCTTCTCATCAAAAGCAAGAGCTACAGACTCTCAGGACA	1390
QY	1381	AGTGTCCACAGGT 1393	
DB	1391	AGTGTCCACAGAT 1403	

RESULT 13

US-10-017-216-1

; Sequence 1, Application US/10017216  
; Publication No. US20020160483A1  
; GENERAL INFORMATION:  
; APPLICANT: KAPILLER-LIBERMANN, Rosana  
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prot  
; TITLE OF INVENTION: Kinase and Uses Therefor  
; FILE REFERENCE: 10147-5701  
; CURRENT APPLICATION NUMBER: US/10/017,216  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/242,429  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 6574  
; TYPE: DNA

; ORGANISM: Homo sapiens									
US-10-017-216-1									
Query Match 93.3%; Score 1381.8; DB 13; Length 6574;									
Best Local Similarity 99.5%; Pred. No. 0;									
Matches 1386; Conservative 0; Mismatches 7; Indels 0; Gaps 0;									
QY	1	TCAAAATATGGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATTGCCAACCGGG	60						
DB	29	TCAAAATATGGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATTGCCAACCGGG	88						
QY	61	CTTCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAACAGCAGATGT	120						
DB	89	CTTCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAACAGCAGATGT	148						
QY	121	CTCCTCTTTCCAGAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGATGCAGTC	180						
DB	149	CTCCTCTTTCCAGAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGATGCAGTC	208						
QY	181	AGCCTGCTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCCGGAAGTATTCGACACCA	240						
; Sequence 10, Application US/10325430									
; Publication No. US20030153525A1									
; GENERAL INFORMATION:									
; APPLICANT: Millennium Pharmaceuticals, Inc									
; APPLICANT: Silos-Santiago, Inmaculada									
; APPLICANT: Rosenfeld, Julie Beth									
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING									
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,									
; FILE REFERENCE: MPI01-294PIRNM									
; CURRENT APPLICATION NUMBER: US/10/325,430									
; CURRENT FILING DATE: 2002-12-19									
; PRIOR APPLICATION NUMBER: US 60/341,953									
; PRIOR FILING DATE: 2001-12-19									
; NUMBER OF SEQ ID NOS: 21									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 10									
; LENGTH: 6574									
; TYPE: DNA									
; ORGANISM: Homo Sapiens									
US-10-325-430-10									
Query Match 93.3%; Score 1381.8; DB 16; Length 6574;									
Best Local Similarity 99.5%; Pred. No. 0;									
Matches 1386; Conservative 0; Mismatches 7; Indels 0; Gaps 0;									
QY	1	TCAAAATATGGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATTGCCAACCGGG	60						
DB	29	TCAAAATATGGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATTGCCAACCGGG	88						
QY	61	CTTCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAACAGCAGATGT	120						
DB	89	CTTCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAACAGCAGATGT	148						
QY	121	CTCCTCTTTCCAGAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGATGCAGTC	180						
DB	149	CTCCTCTTTCCAGAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGATGCAGTC	208						
QY	181	AGCCTGCTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCCGGAAGTATTCGACACCA	240						



Db 209 AGCTGCTCTGATGAAGATTAAAGCACGTGAGCAACTTTGTCCGGAAGATTATCCGACACCA 268  
Qy 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGCAAGGACTTTCGAAGTCAGAGCTTGTGTAG 300  
Db 269 TAGCTGAGTTACAGGAGCTCCAGCCTTCGCAAGGACTTTCGAAGTCAGAGCTTGTGTAG 328  
Qy 301 GTTGTGCTCACTTTGCTGAAAGTGCAGGTGTAGAGAGAAAGCAACCGGGGACATCTATG 360  
Db 329 GTTGTGCTCACTTTGCTGAAAGTGCAGGTGTAGAGAGAAAGCAACCGGGGACATCTATG 388  
Qy 361 CTATGAAAGTATGAAGAAAGAGCTTTATTTGCCCCAGGAGAGCTTTTCAATTTTGTAGG 420  
Db 389 CTATGAAAGTATGAAGAAAGAGCTTTATTTGCCCCAGGAGAGCTTTTCAATTTTGTAGG 448  
Qy 421 AAGAGCGGAACATATTTCTCGAAGCAAGACCCGCTGGATCCGCCAATTACAGTATGCCT 480  
Db 449 AAGAGCGGAACATATTTCTCGAAGCAAGACCCGCTGGATCCGCCAATTACAGTATGCCT 508  
Qy 481 TTCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCTTGGAGGGGACTTGTCTGT 540  
Db 509 TTCAGGACAAAATCACCTTTATCTGATGAGGAAATATCAGCTTGGAGGGGACTTGTCTGT 568  
Qy 541 CACTTTTGAATAGATAGAGGACCAAGTTAGATGAAACCTTGATACAGTTTTTACCTAGCTG 600  
Db 569 CACTTTTGAATAGATAGAGGACCAAGTTAGATGAAACCTTGATACAGTTTTTACCTAGCTG 628  
Qy 601 AGCTGATTTTGGCTGTTTCAGAGCTTTCATCTGATGGATACGTGTCATCGAGACATCAAGC 660  
Db 629 AGCTGATTTTGGCTGTTTCAGAGCTTTCATCTGATGGATACGTGTCATCGAGACATCAAGC 688  
Qy 661 CTGAGAACATTTCTGTTGACCGCAGCAGACACATCAAGCTGGTGGATTTTGGATCTGCGG 720  
Db 689 CTGAGAACATTTCTGTTGACCGCAGCAGACACATCAAGCTGGTGGATTTTGGATCTGCGG 748  
Qy 721 CGAAATGAATTCAAACAAGATGATGTAATCCAACTCCCGATTTGGACCCCAAGATTACA 780  
Db 749 CGAAATGAATTCAAACAAGATGATGTAATCCAACTCCCGATTTGGACCCCAAGATTACA 808  
Qy 781 TGCTCTCTGAAGTCTGACTGTGATGACCGGGATGAAAGGACCACTACGGCTGGACT 840  
Db 809 TGCTCTCTGAAGTCTGACTGTGATGACCGGGATGAAAGGACCACTACGGCTGGACT 868  
Qy 841 GTGACTGGTGTGAGTGGGCGTGAATTCCTATGAGATGATTTATGGAGATCCCCCTTCG 900  
Db 869 GTGACTGGTGTGAGTGGGCGTGAATTCCTATGAGATGATTTATGGAGATCCCCCTTCG 928  
Qy 901 CAGAGGAACTCTGCGAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAT 960  
Db 929 CAGAGGAACTCTGCGAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAT 988  
Qy 961 TTCAGATGACCCCAAGTGAAGTGAATTTCTTGTGATCTGATTCAGAGCTTTGTGTGG 1020  
Db 989 TTCAGATGACCCCAAGTGAAGTGAATTTCTTGTGATCTGATTCAGAGCTTTGTGTGG 1048  
Qy 1021 GCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGTGCTGCCATCCTTCTCTCTAAAATTG 1080  
Db 1049 GCAGAAAGAGAGACTGAAGTTTGAAGGTCTTGTGCTGCCATCCTTCTCTCTAAAATTG 1108  
Qy 1081 ACTGGAAACAATTCGTAATCTCTCCCTCCCTTCTGTTCCCACTCAAGTCCGAGATG 1140  
Db 1109 ACTGGAAACAATTCGTAATCTCTCCCTCCCTTCTGTTCCCACTCAAGTCCGAGATG 1168  
Qy 1141 ACACCTCAATTTTGAAGAACCAAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1200  
Db 1169 ACACCTCAATTTTGAAGAACCAAGAGAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1228  
Qy 1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTTCGTACAGCAAGG 1260  
Db 1229 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTTCGTACAGCAAGG 1288  
Qy 1261 CACTGGGATTTCTTGTAGATCTGAGTCTGTGTGTGTCGGGTCTGGAATCCCTCCGCAAGA 1320  
Db 1289 CACTGGGATTTCTTGTGTAGATCTGAGTCTGTGTGTGTCGGGTCTGGAATCCCTCCGCAAGA 1348

Qy 1321 CTAGCTCCATGGAAAAAGAACTTCTCATCAAAAGCAAGAGCTTCAAGACTCTCAGGACA 1380  
Db 1349 CTAGCTCCATGGAAAAAGAACTTCTCATCAAAAGCAAGAGCTTCAAGACTCTCAGGACA 1408  
Qy 1381 AGTGTCAACAAGGT 1393  
Db 1409 AGTGTCAACAAGAT 1421

## RESULT 15

US-10-757-262-51  
; Sequence 51, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karicheti, Venkateswarlu  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Eliasof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,  
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,  
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,  
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,  
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,  
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,  
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,  
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
; TITLE OF INVENTION: 55053  
; FILE REFERENCE: MPI03-007PIRNONMIN  
; CURRENT APPLICATION NUMBER: US/10757,262  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/478,742  
; PRIOR FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/488,529  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/491,156  
; PRIOR FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 60/499,594  
; PRIOR FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US 60/506,332  
; PRIOR FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 6574  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (19)...(6180)  
US-10-757-262-51

Query Match 93.3%; Score 1381.8; DB 18; Length 6574;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1386; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TCAATATGAGCGCGGAATCCTTTTGGATGCTGTGCTGAACCCCAATTCACACCGGG 60  
Db 29 TCAATATGAGCGCGGAATCCTTTTGGATGCTGTGCTGAACCCCAATTCACACCGGG 88  
Qy 61 CCTCCAGGCTGAATCTGTTCTCCAGGGGAACCAACCCCTTTATGACTCAACAGCAGATGT 120  
Db 89 CCTCCAGGCTGAATCTGTTCTCCAGGGGAACCAACCCCTTTATGACTCAACAGCAGATGT 148



Qy	121	CTCCTCTTTCCCGAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGATGCAGTC	180
Db	149	CTCCTCTTTCCCGAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGATGCAGTC	208
Qy	181	AGCTGCTCTGATGAAGATTAAACGCTGAGCAACTTTGTCCGGAAGTATTCGACACCA	240
Db	209	AGCTGCTCTGATGAAGATTAAACGCTGAGCAACTTTGTCCGGAAGTATTCGACACCA	268
Qy	241	TAGCTGAGTTACAGGAGCTCCAGCTTTCGGCAAGGACTTCGAAGTCAGAAAGTCTGTAG	300
Db	269	TAGCTGAGTTACAGGAGCTCCAGCTTTCGGCAAGGACTTCGAAGTCAGAAAGTCTGTAG	328
Qy	301	GTTGTGGTCACTTTGCTGAGTGCAGTGGTAAAGAGAAAGCAACCGGGGACATCTATG	360
Db	329	GTTGTGGTCACTTTGCTGAGTGCAGTGGTAAAGAGAAAGCAACCGGGGACATCTATG	388
Qy	361	CTATGAAGTGATGAAGAGAGGCTTTATTGCCCCAGGAGCAGGTTTCATTTTTGAGG	420
Db	389	CTATGAAGTGATGAAGAGAGGCTTTATTGCCCCAGGAGCAGGTTTCATTTTTGAGG	448
Qy	421	AAGAGCGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTACAGTATGCCT	480
Db	449	AAGAGCGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTACAGTATGCCT	508
Qy	481	TTCAGGACAAAAATCACCTTTATCTGTCATGGAATATCAGCCTGGAGGGGACTTGTCTGT	540
Db	509	TTCAGGACAAAAATCACCTTTATCTGATGGAGGAATATCAGCCTGGAGGGGACTTGTCTGT	568
Qy	541	CACCTTTGAATAGATATGAGGACCAAGTATGATGAATGAACCTGTATACCTAGCTG	600
Db	569	CACCTTTGAATAGATATGAGGACCAAGTATGATGAATGAACCTGTATACCTAGCTG	628
Qy	601	AGCTGATTTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTGATCGAGATCAAGC	660
Db	629	AGCTGATTTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTGATCGAGATCAAGC	688
Qy	661	CTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG	720
Db	689	CTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG	748
Qy	721	CGAAATGAATTCAAACAGATGGTGAATGCCAAACTCCCGATTTGGGACCCACAGATTACA	780
Db	749	CGAAATGAATTCAAACAGATGGTGAATGCCAAACTCCCGATTTGGGACCCACAGATTACA	808
Qy	781	TGGCTCCTGAAGTGTGACTGTGATGAACGGGATCGAAAGGCACCTACGGCCTGGACT	840
Db	809	TGGCTCCTGAAGTGTGACTGTGATGAACGGGATCGAAAGGCACCTACGGCCTGGACT	868
Qy	841	GTGACTGGTGGTCAGTGGGCGTGATTGCCCTATGAGATGATTTATGGGAGATCCCCCTTCG	900
Db	869	GTGACTGGTGGTCAGTGGGCGTGATTGCCCTATGAGATGATTTATGGGAGATCCCCCTTCG	928
Qy	901	CAGAGGGAACCTCTGCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAT	960
Db	929	CAGAGGGAACCTCTGCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAT	988
Qy	961	TTCCAGATGACCCCAAGTGAGCAGTGTCTTTCTGATCTGATTTCAAAGCTTGTGTGGC	1020
Db	989	TTCCAGATGACCCCAAGTGAGCAGTGTCTTTCTGATCTGATTTCAAAGCTTGTGTGGC	1048
Qy	1021	GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCTTTCTCTTAAATTTG	1080
Db	1049	GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCTTTCTCTTAAATTTG	1108
Qy	1081	ACTGGAACAAATTCGTAACTCTCTCCCTCCCTTCGTTCACCCCTCAAGTCGACGATG	1140
Db	1109	ACTGGAACAAATTCGTAACTCTCTCCCTCCCTTCGTTCACCCCTCAAGTCGACGATG	1168
Qy	1141	ACACCTCCAAATTTTGATGAACAGAGAGAAATTCGTGGGTTTCATCTCTCGTGCAGC	1200
Db	1169	ACACCTCCAAATTTTGATGAACAGAGAGAAATTCGTGGGTTTCATCTCTCGTGCAGC	1228

Qy	1201	TGAGCCCCCTCAGGCTTTCGCGGTGAAGAACTGCCGTTTGTGGGTTTTTCGTACAGCAAGG	1260
Db	1229	TGAGCCCCCTCAGGCTTTCGCGGTGAAGAACTGCCGTTTGTGGGTTTTTCGTACAGCAAGG	1288
Qy	1261	CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTGCGGCTCTGGACTCCCTGCCAAGA	1320
Db	1289	CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTGCGGCTCTGGACTCCCTGCCAAGA	1348
Qy	1321	CTAGCTCCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA	1380
Db	1349	CTAGCTCCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACA	1408
Qy	1381	AGTGTCACAAGGT	1393
Db	1409	AGTGTCACAAGAT	1421

Search completed: March 19, 2005, 18:10:57  
Job time : 813.2 secs

**This Page Blank (uspto)**

Result No.	Score	Match	Query	Length	DB	ID	Description
1	1481	100.0	1515	4	US-09-804-471A-1	Sequence 1, Appli	
2	1481	100.0	1515	4	US-10-238-709-1	Sequence 1, Appli	
3	1388.2	93.7	5877	4	US-10-028-946-3	Sequence 3, Appli	
4	1388.2	93.7	6165	4	US-10-028-946-1	Sequence 1, Appli	
5	947.2	64.0	2162	4	US-09-774-528-419	Sequence 419, Appli	
6	744.8	50.3	1133	4	US-09-916-204-1	Sequence 1, Appli	
7	744.8	50.3	1133	4	US-10-282-048-1	Sequence 1, Appli	
8	234.6	15.8	2423	4	US-09-949-016-2640	Sequence 2640, Appli	
9	225.6	15.2	2726	2	US-08-422-699A-12	Sequence 12, Appli	
10	225.6	15.2	2726	2	US-08-422-706B-8	Sequence 8, Appli	
11	218.8	14.8	2511	2	US-08-422-699A-8	Sequence 8, Appli	
12	218.8	14.8	2511	2	US-08-422-706B-8	Sequence 8, Appli	
13	218.4	14.7	3182	1	US-08-484-044-11	Sequence 11, Appli	
14	205	13.8	174493	4	US-09-804-471A-3	Sequence 3, Appli	
15	205	13.8	174493	4	US-10-238-709-3	Sequence 3, Appli	
16	194	13.1	2706	2	US-08-030-822A-61	Sequence 61, Appli	
17	194	13.1	2706	2	US-09-005-069-61	Sequence 61, Appli	
18	194	13.1	2706	3	US-09-171-158A-20	Sequence 20, Appli	
19	194	13.1	2706	4	US-09-004-730A-20	Sequence 20, Appli	
20	194	13.1	2706	4	US-08-981-799A-20	Sequence 20, Appli	
21	186	12.6	4363	2	US-08-685-576-5	Sequence 5, Appli	
22	184.4	12.5	4848	4	US-09-976-594-295	Sequence 295, Appli	
23	178.8	12.1	48763	4	US-09-916-204-3	Sequence 3, Appli	
24	178.8	12.1	48763	4	US-10-282-048-3	Sequence 3, Appli	
25	175.4	11.8	4065	4	US-09-016-434-1105	Sequence 1105, Appli	
26	175.4	11.8	4739	3	US-08-685-871-1	Sequence 1, Appli	
27	171.6	11.6	5053	2	US-08-685-576-2	Sequence 2, Appli	







Db 1331 CTAGCTCCATGGAAAGAACTTCTCATCAAAAGCAAGAGCTACAGAGCTCTCAGGACA 1390  
Qy 1381 AGTGTCACAGGT 1393  
Db 1391 AGTGCACAGAT 1403

RESULT 5

US-09-774-528-419  
; Sequence 419, Application US/09774528  
; Patent No. 6743619  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyang  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Yonghong  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Dmanac, Radoje T.  
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and  
; FILE OF INVENTION: Polypeptides  
; FILE REFERENCE: 802  
; CURRENT APPLICATION NUMBER: US/09/774, 528  
; CURRENT FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 441  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 419  
; LENGTH: 2162  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (364)..(2010)  
US-09-774-528-419:

Query Match 64.0%; Score 947.2; DB 4; Length 2162;  
Best Local Similarity 99.7%; Pred. No. 8e-310;  
Matches 949; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAACCCATTGCCAACCGGG 60  
Db 374 TCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAACCCATTGCCAACCGGG 433  
Qy 61 CCTCCAGGCTGAATCTGTTCTCCAGGGAAACCCCTTTATGACTCAACAGCATGT 120  
Db 434 CCTCCAGGCTGAATCTGTTCTCCAGGGAAACCCCTTTATGACTCAACAGCATGT 493  
Qy 121 CTCTCTTTCCGAGAGGATATATGATCCCTCTTTGTTCTTTGAAGATGCAGTC 180  
Db 494 CTCTCTTTCCGAGAGGATATATGATCCCTCTTTGTTCTTTGAAGATGCAGTC 553  
Qy 181 AGCTGCTCTGATCAAGATTAAGCAGCTGAGCAACTTTGTCGGAAGTATTCGACACCA 240  
Db 554 AGCTGCTCTGATCAAGATTAAGCAGCTGAGCAACTTTGTCGGAAGTATTCGACACCA 613  
Qy 241 TAGCTGATTAAGAGAGCTCCAGCTTCGGAAGGATTCGAGTCAAGTCTGTGTAG 300  
Db 614 TAGCTGATTAAGAGAGCTCCAGCTTCGGAAGGATTCGAGTCAAGTCTGTGTAG 673  
Qy 301 GTTGTGCTCACTTTGCTGAAGTGCAGTGTAAAGAGAAAGCAACCGGGACATCTATG 360  
Db 674 GTTGTGCTCACTTTGCTGAAGTGCAGTGTAAAGAGAAAGCAACCGGGACATCTATG 733  
Qy 361 CTATGAAGATGATCAAGAAAGGCTTTATTTGGCCAGGAGGAGTTTCAATTTTGGAGG 420

Db 734 CTATGAAGTGTATGAAGAAGAGCTTTATTTGGCCAGGAGAGGTTTTCATTTTGGAG 793  
Qy 421 AAGAGCGGAACATATTTATCTCGAAGCACAGCCCGTGGATCCCCCAATTAACAGTATGCCT 480  
Db 794 AAGAGCGGAACATATTTATCTCGAAGCACAGCCCGTGGATCCCCCAATTAACAGTATGCCT 853  
Qy 481 TTCAGGACAAAAATCACCTTTATCTGGTCAATGGAATATCAGCCTGGAGGAGATTTGCTGT 540  
Db 854 TTCAGGACAAAAATCACCTTTATCTGGTCAATGGAATATCAGCCTGGAGGAGATTTGCTGT 913  
Qy 541 CACTTTTGAATAGATATGAGGACCATAGATGAAAACCTGATACAGTATTTACCTAGCTG 600  
Db 914 CACTTTTGAATAGATATGAGGACCATAGATGAAAACCTGATACAGTATTTACCTAGCTG 973  
Qy 601 AGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGGATACGTCGATCGAGACATCAAGC 660  
Db 974 AGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGGATACGTCGATCGAGACATCAAGC 1033  
Qy 661 CTGAGAACATTTCTCGTTGACCCGACAGGACATCAAGCTGGTGGATTTTGGATCTGCCG 720  
Db 1034 CTGAGAACATTTCTCGTTGACCCGACAGGACATCAAGCTGGTGGATTTTGGATCTGCCG 1093  
Qy 721 CGAAATGAATTCAAAACAAGATGCTGAATGCCAAAACCTCCCGATTTGGACCCAGATACA 780  
Db 1094 CGAAATGAATTCAAAACAAGATGCTGAATGCCAAAACCTCCCGATTTGGACCCAGATACA 1153  
Qy 781 TGGCTCTCGAAGTGTGACTGTGATGAACGGGGATGGAAGACACCTACGGCTGGACT 840  
Db 1154 TGGCTCTCGAAGTGTGACTGTGATGAACGGGGATGGAAGACACCTACGGCTGGACT 1213  
Qy 841 GTGACTGGTGGTCACTGGGCGTGAATTCCTTATGAGATGATTTATGGAGATCCCCCTTCG 900  
Db 1214 GTGACTGGTGGTCACTGGGCGTGAATTCCTTATGAGATGATTTATGGAGATCCCCCTTCG 1273  
Qy 901 CAGAGGAACCTCTGCCAGAACCTTCAATTAACATTTATGATTTCCAGCGGTT 952  
Db 1274 CAGAGGAACCTCTGCCAGAACCTTCAATTAACATTTATGATTTCCAGGTT 1325

RESULT 6

US-09-916-204-1  
; Sequence 1, Application US/09916204  
; Patent No. 6638745  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164CIP  
; CURRENT APPLICATION NUMBER: US/09/916,204  
; CURRENT FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1133  
; TYPE: DNA  
; ORGANISM: Human  
US-09-916-204-1

Query Match 50.3%; Score 744.8; DB 4; Length 1133;  
Best Local Similarity 99.7%; Pred. No. 2.2e-241;  
Matches 746; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 TCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAACCCATTGCCAACCGGG 60  
Db 64 TCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAACCCATTGCCAACCGGG 123  
Qy 61 CCTCCAGGCTGAATCTGTTCTCCAGGGAAACACCCCTTTATGACTCAACAGCAGATGT 120  
Db 124 CCTCCAGGCTGAATCTGTTCTCCAGGGAAACACCCCTTTATGACTCAACAGCAGATGT 183  
Qy 121 CTCTCTTTCCGAGAGGATATATGATCCCTCTTTGTTCTTTTGAAGAATGCAGTC 180







184	CTGCTCTGATGAAGATTAA	CGCATGCTGCGAAGTATT	TCGGACACCATAG	243
243	CCGAACTGGGCCAGGACA	AGTACGTCGGCCGACCT	TTCGAGTGGCGGAGCCCAT	302
244	CTGAGTTACAGGAGCTCC	AGCCTTCGGCAAGACCT	TCGAAAGTCAGAGTCT	303
303	TGAGGCTTTAAGGAGGTC	CCGACTCCAGAGGACAC	TTCGAGATTCCTGAAGTGAT	362
304	GTGCTCACCTTTGCTGA	GTGTCAGGTGTAAGAGAA	AGCAACGGGGACATCTAT	363
363	CGCGGGCGTTACGAGAG	TAGCGTAGTGAAGATGA	AGCAGACGGGCCAGGTGT	422
364	TGAAAGTGATGAAGAGA	AGGCTTTATTTGCCCGC	AGAGCAGAGTTTATTTT	423
423	TGAAGATCATGAACAAG	ATGGGACATGCTGAAGAG	GGGCGAGGTGTCTGCT	482
424	AGCGGAACATATTATCT	CGAAGCACAGCCGTGG	ATCCCCCAATTACAGTAT	483
483	AGAGGGACGTGTTGGT	GAATGGGGAACGGCGGT	TGGATCAGCAGCTTGC	542
484	AGGACAAAATACCTTT	ATCTCGTCATGGAATAT	CAGCCTTGAGGGGACT	543
543	AGGATGAGAACTACCT	GTACTCGTCATGAGTAT	TACGTGGCGGGGACCT	602
544	TTTTTGAATAGATAGGA	CCAGTTAGATGAAGAACT	GATACAGTTTACTTAC	603
603	TGCTTGACCAAGTTGG	GAGCGGATTCGGCCCG	AGATGGCGCGCTTAC	662
604	TGATTTTGGCTGTTCAG	CGGCTTCATCTGATGGG	ATACGTGCATCGAGAC	663
663	TTGTTCATGGCCATAG	ACTCGGTGCAACGGCT	TGGCTACGTGCACAGG	722
664	AGAACTTCCTGTTGAC	CGGCACAGGACACAT	CAAGCTGGTGGATTT	723
723	ACAACATCTCTGACCG	CTGTGGCCACATCCGC	CTGGCGGACTTCTG	782
724	AAATGAATTCAAACAG	ATGGTGAATGCCAACT	CTCCGATTTGGGACCC	783
783	AGCTGCGGGCAGAT	TGAAACGGTGGCTGC	TGTGGGACCCCAAGAT	842
784	CTCCTGAAGTGTCTGA	---CTGTGATGAACGGG	ATGGAAGGCACCTAC	840
843	CCCCGAGATCCTGC	AGGCTGTGGCGGTGG	CTGGGACAGCAGCTAC	902
841	GTGACTGGTGGTCA	TGTGGGCGTGAATCC	CTATGAGATGATTTAT	900
903	GTGACTGGTGGGCGCT	GGGTGTATTCGCCCT	ATGAAATGTTCTATGG	962
901	CAGAGGGAACTCTGC	AGAACCTTCAATAACAT	TATGAATTTCCAGCGG	960
963	ACGCGGATTCACCG	CGGAGACCTATGGCA	AGATCGTCCACTACAG	1022
961	TTCCAGATGACCCCAA	AGTGAGCAGT---GAC	TTTTCATCTGATTTCA	1017
1023	TGCCGTGGTGGACGA	AGGGGTCCCTGAGGAG	GTCCGAGACTTCATTC	1082
1018	CGCGCCAGAAGAGAG	ACTGAAATTTGAAAGT	CTTTGCTGCG-----	1068
1083	GTCCCCCGGAGACAC	GGCTGGGCGGGTGAG	GAGCGGACTTCCGAG	1142
1069	TCTCTAAATTTGACTG	GAAACAACATTCGTAA	CTCTCCCTCCGTTCC	1128
1143	TCITTTGGCTCGACTG	GGATGGTCTCGGGAC	AGCGGTGCCCCCTT	1202
1129	AGTCCGACGATGAC	CACTCCAAATTTTGA	1156	
1203	AAGTGGCACCGGACA	CATGCACTTCGA	1230	

```

; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harlev, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02713
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,706B
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,543
; FILING DATE: 08-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,612
; FILING DATE: 26-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/839,255
; FILING DATE: 20-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01545
; FILING DATE: 19-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00253
; FILING DATE: 05-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB9202485.0
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5830A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-422-706B-12

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RESULT 10  
US-08-422-706B-12  
; Sequence 12, Application US/08422706B  
; Patent No. 5977333

364	QY	TGAAAGTGTAGAAAGAAAGCCTTTATTGGCCCAAGAGCAGGTTTCATTTTTTTGAGGAAG	423
423	DB		
423	DB	TGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGGAGGTGTCGTGCTTCGTTGAGG	482
424	QY	AGCGGAACATATTATCTCGAAGCACAAAGCCGCTGGATCCCCCAATTACAGTATGCTTTC	483
483	DB		
483	DB	AGAGGACGTGTTGGTGAATGGGACCGCGGTGGATCACGACGTGCACCTTCGCTTC	542
484	QY	AGGACAAAATCACCTTTATCTGGTCATGAATATCAGCTGAGGGGAGCTTGGTGTAC	543
543	DB		
543	DB	AGGATGAGAACTACCTGTACTGTCGTATGAGATATTACGTGGGCGGGGACCTGCTGACAC	602
544	QY	TTTTTGAATAGATATGAGGACAGTTAGATGAAAACCTGATACAGTTTTTACTAGCTGAGC	603
603	DB		
603	DB	TGCTGAGCAAGTTTGGGAGCGGATTCGGGCCGAGATGGCGCGCTTCTACTGGCGAGA	662
604	QY	TGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGATCGATCGAGACATCAAGCCTG	663
663	DB		
663	DB	TTGTCTATGGGCATAGACTCGGTGTCACCGGCTTGGCTACGTGTCACAGGGACATCAAAACCG	722
664	QY	AGAACTTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCGCGGA	723
723	DB		
723	DB	ACAACATCTCTGTGACCGCTGTGGCCACATCGCCTGGCCGACTTCGGCTCTTGGCTCA	782
724	QY	AAATGAATTCAAAACAGATGGTGAATGCCAAACTCCGATTTGGGACCCCAAGATTCATATGG	783
783	DB		
783	DB	AGCTCGGGGAGATGGAAACGGTGGCTGCTGGTGGCTGTGGGACACCCACAGACTACCTGT	842
784	QY	CTCTGAAGTGCTGA---CTGTGATGAACGGGGATGGAAGGCACCTACGGCTGGACT	840
843	DB		
843	DB	CCCCGAGATCTCTGACGCTGTGGCGGTGGGCCCTGGGACAGGCAGCTACGGGCCGAGT	902
841	QY	GTGACTGGTGGTCTAGTGGGGGTGATTGCCCTATGAGATGATTTATGGGAGATCCCCCTTCG	900
903	DB		
903	DB	GTGACTGGTGGCGCTGGGTGATTCCCTATGAAATGTTCTATGGGCAGACGCCCTTCT	962
901	QY	CAGAGGAACTCTGCCAGAACCTTCAATTAACATTATGAATTTCCAGCGGTTTTTGAAT	960
963	DB		
963	DB	ACGCGGATTCACGGCGGAGACCTATGGCAAGATCGTCCACTACAGGAGACCTCTCTC	1022
961	QY	TTCCAGATGACCCCAAGTAGCAGCAGT---GACTTTTCTTGATCTGATTCAAAGCTTGTGT	1017
1023	DB		
1023	DB	TGCGCTGTTGGACGAAGGGTCCCTGAGGAGGCTCGAGACTTCATTACAGCGTTGCTGT	1082
1018	QY	GGCGCCAGAAGAGAGACTGAAGTTTGAAGTCTTTGCTGG-----CATCTTTTCT	1068
1083	DB		
1083	DB	GTCCCCCGGAGACACCGCTGGCGGGGTGGAGCAGCGACTTCCGGACACATCCCTTCT	1142
1069	QY	TCTCTAAATTTGACTGGAACAAACATTTCGTAACTCTCTCCCGCTTGGTCCCAACCTCA	1128
1143	DB		
1143	DB	TCTTTGGCTCGACTGGATGGTCTCGGAGACAGCGTGCCCGCTTTTACACCGGATTCG	1202
1129	QY	AGTCCGACGATGACACTCCAAATTTGA	1156
1203	DB		
1203	DB	AAGGTGCCACCGACACATGCACTTCA	1230

## RESULT 11

RESULTS  
US-08-422-699A-8

US 00 422 035A 0  
: Sequence 8, Application US/08422699A

: Patent No. 5955265

GENERAL INFORMATION:

APPLICANT: Brook, J. David

APPLICANT: Housman, David E.

APPLICANT: Shaw, Duncan J.

APPLICANT: Harley, Helen G.

APPLICANT: Johnson, Keith

**TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC**

**TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF**

NUMBER OF SEQUENCES: 14

; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:

ADDRESS: Hamilton. Brook. Smith & Reynolds. P.C.

STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02713  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422.699A

NAME/KEY: CDS  
LOCATION: 1..1746

Query Match

Query Match  
Best Local Similarity 14.8%, Score 210.0, DB 2, Length 2011,  
Pred. No. 1e-62:

BEST LOCAL SIMILARITY 34.3%; FREQ. NO. 1E-62;  
Matches 511: Conservative 0: Mismatches 412: Indels 15: Gaps 3:

234 GACACCATAGCTGAGTTACAGGAGCTCCAGCCCTTCGGCAAAGGACTTCGAAGTCAGAAAGT 293

db 43 GCCATCGTGGTGAGGCCTTAAGGAGGTCGCACTGCAGAGGGACGACTTTCGAGATTTCTGAAG 102

294 CTTGTAGGTTCTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGGGAC 353

db 103 GTGATCGGACCGCGGGCGTTCAGCGAGGTAGCGGTAGTGAAGCAGACGGGCCAG 162

354 ATCTATGCTATGAAAGTGATGAAGAAGGCTTTATTGGCCAGGAGCAGGTTTCATT 413

Db 163 GTGTATGCCATGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGCGAGGTGTCGTGC 222

414 TTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTACAG 473

Db 223 TTCCGTGAGGAGGGACGTGTTGGTGAA TGGGGACCGGGCGGTGGATCACGCAGCTGCAC 282

474 TATGCCCTTTCAGGACAAAAATCACCTTTATCTGGTCAATATCAGCCTGGAGGGGAC 533

Db 283 TTGCGCTTCCAGGATGAGAACTACCTGTACTGCTCATGAGTATTACGTGGCGGGAC 342  
Qy 534 TTGCTGTCACTTTTGAATAGATAGAGACAGTTAGTAAACCTGATACAGTTTAC 593  
Db 343 CTGCTGACACTGCTGAGCAAGTTTGGGAGCGGATTCGGCCGAGATGGCGCTTCTAC 402  
Qy 594 CTAGCTGAGCTGATTTTGGCTGTTTACAGGCTTCATCTGATGGATAGCGTGCATCGAGAC 653  
Db 403 CTGGCGGAGATTGTATGGCCATAGATCTGGTGACCGGCTTGGCTACGTCAGGAGAC 462  
Qy 654 ATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGA 713  
Db 463 ATCAAAACCCGACAACTCTGCTGACCGCTGTGGCCACATCCGCTTGGCGGCTTGGC 522  
Qy 714 TCTGCCCGGAAATGAATTCAAACAGATGGTGAATGCCAACTCCCGATGGGACCCCA 773  
Db 523 TCTTGCTCAAGCTGCGGGGAGATGGAACGCTGGCTGCTGGTGGCTGTGGGCACCCCA 582  
Qy 774 GATTACATGGCTCTGA--AGTCTGACTGTGATGAACGGGATGGAAGGACACCTAC 830  
Db 583 GACTACTGTCCCCGAGATCTGACGCTGTGGCGGTGGGCTGGGACAGGAGCTAC 642  
Qy 831 GGCCTGACTGTGACTGTGGTGTGAGTGGGCTGATTCCTATGAGATGATTTATGGGAGA 890  
Db 643 GGGCCGAGTGTGACTGTGGGCTGGGTATTCGCTATGAATGTTCTATGGGAG 702  
Qy 891 TCCGCTTCCGAGGGAACCTCTGCCAGAACCTTCAATTAACATTATTAATTTCCAGCGG 950  
Db 703 ACGCCCTTCTACGGGATTCACGGCGGAGACCTATGGCAAGATCGTCCACTACAAGGAG 762  
Qy 951 TTTTGAATTTCCAGATGACCCCAAGTGAGCAGT--GACTTTTGTGATCTGATTCAA 1007  
Db 763 CACTCTCTCTGCGCTGTGGAGGAAGGGTCCCTGAGAGGCTCAGACTTCATTCAG 822  
Qy 1008 AGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGC----- 1058  
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Qy 1059 CATCTTTCTCTCTATAAATTGACTGGAACAACTTGTAACTCTCTCCCGCTTCTGTT 1118  
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Db 943 CCGGATTCGAAGTGCACCGACACATGCACTTGA 980

RESULT 12  
US-08-422-706B-8  
; Sequence 8, Application US/08422706B  
; Patent No. 5977333  
; GENERAL INFORMATION:  
; APPLICANT: Brook, J. David  
; APPLICANT: Housman, David E.  
; APPLICANT: Shaw, Duncan J.  
; APPLICANT: Harley, Helen G.  
; APPLICANT: Johnson, Keith J.  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC  
; TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02713  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/422,706B  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/284,543  
; FILING DATE: 08-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/023,612  
; FILING DATE: 26-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/839,255  
; FILING DATE: 20-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/01545  
; FILING DATE: 19-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/00253  
; FILING DATE: 05-FEB-1993  
; PRIOR APPLICATION DATA: GB9202485.0  
; APPLICATION NUMBER: 06-FEB-1992  
; FILING DATE: 06-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: MIT-5830A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2511 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1746  
; US-08-422-706B-8

Query Match 14.8%; Score 218.8; DB 2; Length 2511;  
Best Local Similarity 54.5%; Pred. No. 1e-62;  
Matches 511; Conservative 0; Mismatches 412; Indels 15; Gaps 3;

Qy 234 GACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCAAGAGCACTTCGAGTCAGAGT 293  
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Qy 294 CTTGTAGGTGTGCTCACTTTTGTGAAGTGCAGGTGCTAAGAGAGAAAGCAACCGGGAC 353  
Db 103 GTGATCGGACGCGGGCGTTTCAGCGAGGTAGCGGTAGTGNAGATGAAGACAGCGGCCAG 162  
Qy 354 ATCTATGCTATGAAGTGTATGAAGAGAGGCTTTATTTGGCCCGAGGACGAGTTTCATTT 413  
Db 163 GTGTATGCTATGAAGTGTATGAAGAGAGGCTTTATTTGGCCCGAGGAGGCTGCTGTC 222  
Qy 414 TTTGAGAGAGCGGAGCAATATTTATCTCGAAGCACAAGCCCGTGGATCCCGCAATTACAG 473  
Db 223 TTCCGTTGAGGAGGAGCGGCTGTTGGTGAATGGGACCGCGGTGGATCAGCGAGCTGCAC 282  
Qy 474 TATGCCCTTTGAGGACAAATACCTTTTATCTGGTCAATGAATATCAGCCTCGAGGGGAC 533  
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Db 403 CTGGCGGAGATTGTCAATGGCCATAGACTCGGTGACCGGCTTGGCTACGTCAGGAGAC 462  
Qy 654 ATCAAGCCTGAGAACTATCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGA 713

[illegible]

RESULT 13

US-08-484-044-11

US 66 101 011 11  
; Sequence 11, Application US/08484044

; Patent No. 5552282

GENERAL INFORMATION:

APPLICANT: Caskey, C. T.

APPLICANT: Fu, Ying-Hui

APPLICANT: Friedman, David L.

APPLICANT: Pizzuti, Antonio

APPLICANT: Fenwick, Raymond G.

**TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy**

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski, L.L.P.

STREET: 1301 McKinney, Suite 5100

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

ZIP: 77010-3095

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

**COMPUTER: IBM PC compatible**

OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,044

FILING DATE:

; CLASSIFICATION: 435

**; PRIOR APPLICATION DATA:**

APPLICATION NUMBER: US 08/019,940

FILING DATE: 19-FEB-1993

;  
;  
; ATTORNEY/AGENT INFORMATION:

NAME: Paul, Thomas D.

REGISTRATION NUMBER: 32,714

REFERENCE/DOCKET NUMBER: D-5443

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/651-5325

TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3182 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-484-044-11

Query Match 14.7%; Score 218.4; DB 1; Length 3182;

Best Local Similarity 54.5%; Pred. No. 1.6e-62;

Matches	510;	Conservative	0;	Mismatches	411;	Indels	15;	Gaps	3;
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Qy	236	CACCATAGCTGAGTTACAGAGCTCCAGCCTTCGGCCAAAGACATTCGAGTGCAGAGTCT	295
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Qy	296	TGTAGGTTGTGGTCACTTTGTCTCAAGTGCAGGTGGTAAGAGAGAAACCAACCGGGGACAT	355
Db	803	GATCGGACGCGGGCGTTTACGCGAGGTAGCGGTAGTGAAGATGAACGAGACGGGCCAGGT	862
Qy	356	CTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCCAGGAGCAGGTTTTCATTTTT	415
Db	863	GTATGCCATGAAGTACATGAACAAGTGGGACATGCTGAAGAGGGCGAGGTGTCGTGCTT	922
Qy	416	TGAGGAGAGCGGAAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTACAGTA	475
Db	923	CCGTGAGGAGAGGACGTTGTGTGAATGGGGACCGGCGGTGGATCACGCAGCTGCACCT	98
Qy	476	TGCTTTTCAGGACAAAAATCACCTTTATCTGCTCATGGAATATCAGCCTCGAGGGGACTT	535
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Qy	536	GCTGTCACTTTTGAATAGATATGAGGACCACTAGTATGAAACCTGATACAGTTTTCACCT	595
Db	1043	GCTGACACTGCTGAGCAAGTTTGGGAGCGGATTCGGGCCGAGATGCGCGCTTCTACCT	1102
Qy	596	AGCTGAGCTGATTTTGGCTGTTACAGCGTTCACTCTGATGGGATACGTGCATCGAGACAT	655
Db	1103	GGCGGAGATTGTATGGCCCATAGACTCGGTGACCCGCTTGGCTACGTGCACAGGGACAT	1162
Qy	656	CAAGCTTGAAACATTTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATC	715
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Qy	776	TTACATGGCTCTGA---AGTGCTGACTGTGATGTAACGGGGATGGAAGGCACCTACGG	832
Db	1283	CTACCTGTCCCCGAGATCCTCGAGGCTGTGGCGGTGGGCCCTGGGACAGCGACGTACGG	1342
Qy	833	CTGGAAGTGAAGTGTGTGCTGAGTGGCGGTGATTGCTATGAGATGATTTATGGGAGATC	892
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Db	1403	GCCTTCTACCGCGAATTCACGCGCGGAGACCTATGGCAAGATCGTCCACTACAAAGGACGA	1462
Qy	953	TTTGAATTTCCAGATGACCCCAAGATGAGCAGT---GACTTTTCTGATCTGATTTCAAAG	1009
Db	1463	CTCTCTCTGCCGCTGGTGACGAAGGGGTCCCTGAGGAGGCTCGAGACTTCATTTACGG	1522
Qy	1010	CTTGTGTGGCGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTTGTGTC-----CA	1060
Db	1523	GTGTGCTGTCTCCCGGAGACAGGCTGGGCGGGGTGGAGCAGGCGACTTCGCGACACA	1582
Qy	1061	TCCTTTCTCTCAAATTTGACTTGGAAACAACATTCGTAACTCTCTCCCTCCCTTCGTTTCC	1120



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 07:45:41 ; Search time 4489.47 Seconds  
(without alignments)  
12556.766 Million cell updates/sec

Title: US-10-724-594-1\_COPY\_17\_1497

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Sequence: 1 tcaatatgagcgcggaat.....ccggggcgctgctggctc 1481

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602.6	40.7	698	5	BP146990
2	521.2	35.2	1085	5	BM904785
3	478	32.3	432	7	CR746615
4	438.4	29.6	600	4	EG808196
5	423.8	28.6	427	4	BG944539
6	409.4	27.6	485	7	CR746792
7	400.4	27.0	617	5	BQ417810
8	380	25.7	481	7	CN682405
9	378	25.5	479	7	CN678533
10	337	22.8	490	2	BF562826
11	329.8	22.3	821	4	B1654262
12	327	22.1	449	9	CG501399
13	325	21.9	450	9	CG501400
14	318.2	21.5	512	9	CG652891
15	314.2	21.2	340	2	BF380737
16	312.8	21.1	423	2	BF344814
17	312.6	21.1	582	5	BX516291
18	281.6	19.0	521	1	AI882189
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24	262.4	17.7	524	7	CK841805

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30	245.8	16.6	647	7	CF744580
31	240.8	16.3	401	6	BY602044
32	238.8	16.1	2688	3	BC024150
33	237.2	16.0	2862	3	BC056615
34	237	16.0	398	5	BY018641
35	236	15.9	1478	9	AY408842
36	235.6	15.9	807	7	CK147448
37	233.6	15.8	605	5	BP168081
38	233.4	15.8	563	6	CD310916
39	233.4	15.8	801	5	BU475240
40	233.4	15.8	847	5	BU467302
41	231.4	15.6	423	2	BB823725
42	231.2	15.6	508	6	CB783081
43	225.2	15.2	1600	3	BC038993
44	218.4	14.7	1472	9	AY408840
45	217.2	14.7	370	5	BY021399

## ALIGNMENTS

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BP146990  
LOCUS  
DEFINITION  
BP146990 full-length enriched swine cDNA library, adult ovary Sus  
scrofa cDNA clone OVRM10025B09 5', mRNA sequence.  
ACCESSION  
BP146990  
VERSION  
BP146990.1 GI:40396461  
KEYWORDS  
EST.  
SOURCE  
Sus scrofa (pig)  
ORGANISM  
Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE  
1 (bases 1 to 698)  
AUTHORS  
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,  
Okumura,N., Hamasima,N. and Awata,T.  
TITLE  
PEDE (Pig EST Data Explorer): construction of a database for ESTs  
derived from porcine full-length cDNA libraries  
JOURNAL  
Nucleic Acids Res. 32 (1), D484-D488 (2004)  
COMMENT  
Contact: Hirohide Uenishi  
Animal Genome Laboratory, Genome Research Department  
National Institute of Agrobiological Sciences  
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
Tel: +81-29-838-8627  
Fax: +81-29-838-8627  
Email: huenishi@affrc.go.jp  
EST project with full-length enriched cDNA libraries carried out in  
Animal Genome Research Program (Japan) by National Institute of  
Agrobiological Sciences and STAFF-Institute  
Single pass sequencing of clones derived from oligo-capped cDNA  
library  
Vector sequences were eliminated by RepeatMasker version 2002/07/13  
and crossmatch version 0.990319  
Low quality bases were trimmed based on the quality values.

Location/Qualifiers  
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/dev\_stage="adult"  
/clone\_lib="full-length enriched swine cDNA library, adult  
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source

Query Match 40.7%; Score 602.6; DB 5; Length 698;  
Best Local Similarity 91.4%; Pred. No. 7.9e-172;  
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Db      461 AGGAGGAAACATATTATCTCGGAGCAGAGTCTCTGGATCCCTTACAGTACGCCT 520
Qy      481 TTGAGGCAAAATCACCCTTTATCTGCTGATGGAATATCAGCTCGAGGGGACCTTGCTGT 540
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Qy      541 CACTTTTGAATAGATGAG 560
Db      581 CGCTTCTGAACAGATACGAG 600

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LOCUS   BG944539
DEFINITION Homo sapiens cDNA clone ax51f11 random, mRNA sequence.
ACCESSION BG944539
VERSION   BG944539.1 GI:14343911
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 427)
AUTHORS Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
TITLE    Gene expression in proliferating human erythroid cells
JOURNAL  Genomics 59 (2), 168-177 (1999)
MEDLINE  99339981
PUBMED   10409428
COMMENT  Contact: Jeffery L. Miller
          Laboratory of Chemical Biology
          National Institute of Diabetes and Digestive and Kidney Diseases
          Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
          20892, USA
          Tel: 301 402 2373
          Fax: 301 435 5148
          Email: jm7f@nih.gov
          DNA Sequencing and analyses by National Institutes of Health
          Intramural Sequencing Center (NISC).
          Plate: 51 row: f column: 11
          Seq primer: -21M13 forward primer (ABI).
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              /lab_host="SOLR"
              /clone_lib="Hembase; Erythroid Progenitor Cells (UCB:ax
              library)"
              /notes="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;
              Site 2: EcoRI; 65,000 proliferating erythroid cells from
              the Buffy coat of a blood donation were obtained by flow
              cytometric separation after a 5-day culture period in the
              presence of erythropoietin. Total RNA was purified from
              the sorted cell population using Trizol reagent. RNA (0.3
              ug) was converted into double stranded cDNA using
              Clontech's CapFinder cDNA Library Construction Kit
              (Clontech) according to the manufacturer's protocol and
              cloned into EcoRI digested Lambda Zap II vector
              (Stratagene). The phage library was amplified once prior
              to in vivo excision in SOLR cells. Individual colonies
              were grown, and the cDNA inserts were sequenced in high
              throughput (NIH intramural sequencing center
              http://www.nisc.nih.gov/)."
FEATURES
source

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Query Match      28.6%; Score 423.8; DB 4; Length 427;
Best Local Similarity 99.5%; Pred. No. 2.4e-117;
Matches 425; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      132 CGAAGAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAAGTGCAGCTGCTCTG 191
Db      1 CGAGAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAAGTGCAGCTGCTCTG 60
Qy      192 ATGAAGATTAAAGCACCGTGAGCAACTTTGTCCCGAAGTATTCCGACACCATAGCTGAGTTA 251
Db      61 ATGAAGATTAAAGCACCGTGAGCAACTTTGTCCCGAAGTATTCCGACACCATAGCTGAGTTA 120
Qy      252 CAGGAGCTCCAGCTTCGGCAAGGACTTCGAGTGCAGAGTCTTGTAGTGTGTTGGTGCAC 311
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Qy      312 TTTGCTGAAAGTGCAGGTGGTAAAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTG 371
Db      181 TTTGCTGAAAGTGCAGGTGGTAAAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTG 240
Qy      372 ATGAAGAAGAGGCTTTATTTGCCCCAGGAGGAGTTTCATTTTTCAGGAAGAGCGGAAC 431
Db      241 ATGAAGAAGAGGCTTTATTTGCCCCAGGAGGAGTTTCATTTTTCAGGAAGAGCGGAAC 300
Qy      432 ATATTATCTCGAGACCAAGCCGTCGATCCCGCAATTACAGTATGCTTTCAGGACAAA 491
Db      301 ATATTATCTCGAAGTACAAGCCGTCGATCCCGCAATTACAGTATGCTTTCAGGACAAA 360
Qy      492 AATCACCTTTATCTGCTCATGGAATATCAGCTTCGAGGGGAGCTTGTGTCACATTTTGAAT 551
Db      361 AATCACCTTTATCTGCTCATGGAATATCAGCTTCGAGGGGAGCTTGTGTCACATTTTGAAT 420
Qy      552 AGATATG 558
Db      421 AGATATG 427

RESULT 6
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LOCUS   CR746792
DEFINITION 485 bp mRNA linear EST 30-AUG-2004
          IMAGE:4149886 5', mRNA sequence.
ACCESSION CR746792.1 GI:51660027
VERSION   CR746792
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 485)
AUTHORS Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
          Peters,M., Radelof,U. and Schneider,D.
          I.M.A.G.E. cDNA Clone Collection
          Unpublished (2004)
TITLE     Contact: Inge Arlart
JOURNAL   RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
          Heubnerweg 6, D-14059 Berlin, Germany
          Email: www.rzpd.de
          RZPD; IMAGp998E239412.
          RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
          Contact: Inge Arlart
          RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH.
          Heubnerweg 6, D-14059 Berlin, Germany
          Tel: +49 30 32639 100
          Fax: +49 30 32639 111
          www.rzpd.de
          This clone is available royalty-free from RZPD;
          contact RZPD (clone@rzpd.de) for further information. Seq primer:
          M13r, Primer sequence: TTTCACAGGAACAGCTATGAC.
FEATURES
source
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[illegible]

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ACCESSION	BQ417810
VERSION	BQ417810.1 GI:21123011
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. 1 (bases 1 to 617)
AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hiller,I., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
TITLE	Endocrine Pancreas Consortium
JOURNAL	Unpublished (2000)
COMMENT	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557

```

Email: dmelton@biohph.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Marie Searce
(mnsearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 367.
Location/Qualifiers
1. .617
/organism="Mus musculus"
/mol_type="mRNA"
/strain="I29/Sv x CD1"
/db_xref="taxon:10090"
/dev_stage="p.c. 14.5"
/lab_host="E. coli-DH12S (GIBCO)"
/clone_lib="Kaeatner ngn3 wt"
/note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
Not I; Site_2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and SalI linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-SalI sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/-. The wt library is in
pSPORT1, T7 promoter is 5'."

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ORIGIN	Query Match	27.0%; Score 400.4; DB 5; Length 617;	
	Best Local Similarity	86.0%; Pred. No. 3.9e-110;	
	Matches 443; Conservative 0; Mismatches 72; Indels 0; Gaps 0;		
Qy	1	TCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGTAACCCATTTGCCAACCGGG	60
Db	103	TCAAGTATGTTGTGCGGAACCCGCGGAGGCCAGTGCCTCCGAGGCCATTTGCCAGTCGGG	162
Qy	61	CTCTCAGGCTGAATCTGTTCTTCCAGGGGAAACCCCTTTATGACTCAACAGCAGATGT	120
Db	163	CTCTCAGGCTAAATCTCTTCTTCCAGGGGAAACCGCCCTCATGACTCAACAGCAGATGT	222
Qy	121	CTCTCTTTTCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAAATGCAGTC	180
Db	223	CTGCTCTTTTCCGGGAAGGGATGCTAGACGCCCTCTTCGCTCTCTTTGAAGAGTGCAGCC	282
Qy	181	AGCCTGCTCTGATGAAGATTAAAGCAGTGAAGCACTTTGTCCGGAAGTATTCGACACCA	240
Db	283	AACCCGCCCTGATGAAGATGAAGACGTGAGCAGCTTTGTTCAGAAAGTATTCGACACCA	342
Qy	241	TAGCTCAGTTTACAGGAGCTCCAGCCCTTCGCGAAAGGACTTTCGAAGTCAGAAGTCTTTGTAG	300
Db	343	TAGCCGAGTTTGGGGAGCTGCGAGCGTTCGCGAGAGACTTCGAAGTTCGAAGCTTTGTG	402
Qy	301	GTGTGCGTCACTTTGCTGAAGTGCAGGTGGTAAAGAGAAAGCAACCGGGGACATCTATG	360
Db	403	GCTGTGCTCACTTCGCTGAAGTGCAGTGGTAAAGAGAAAGCGACCGGGGAGCTCTATG	462
Qy	361	CTATGAAGTGTATGAAGAAGAGGCTTTATTTGGCCGAGGACAGGTTTCATTTTTTGAGG	420
Db	463	CCATGAAATTCATGAAGAAGAAGGCTTTGCTGGCCCGAGGAACAGAGTTTCATTTTTTCGAGG	522
Qy	421	AGAGCGGAACATATTATCTCGAAGCACAAAGCCGCTGGATCCCCCAATTTACAGTATGCCT	480
Db	523	AGAGAGGAACATATTATCTCGAGGACAGGTCCTTTGGATCCCCAGTTACAGTACGCCT	582
Qy	481	TTCAGGACAAAATCAACCTTTATCTGGTCAATGAA	515
Db	583	TTTCAAGGACAAAATAACCTTTTACCTGTCATGAA	617

RESULT 8

CN682405

LOCUS

CN682405

481 bp

mRNA

linear

EST 17-MAY-2004

DEFINITION E0164B04-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long) Mus musculus cDNA clone NIA:E0164B04 IMAGE:30782511 5', mRNA sequence.

ACCESSION CN682405

VERSION CN682405.1 GI:47448856

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases 1 to 481)

AUTHORS Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., VanBuren, V., Falco, G., Martin, P.R., Staggs, C.A., Bassey, U.C., Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelsoe, J., Hide, W. and Ko, M.S.

TITLE Transcriptome analysis of mouse stem cells and early embryos

JOURNAL PLoS Biol. 1 (3), 410-419 (2003)

COMMENT Contact: Dawood B. Dudekula Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: E0164 row: B column: 04 Seq primer: M13 Reverse High quality sequence stop: 481 POLYA=No.

FEATURES

source

1..481

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129Sv/EvTac"

/db\_xref="niaEST:E0164B04-5"

/db\_xref="taxon:10090"

/clone="NIA:E0164B04 IMAGE:30782511"

/sex="Male"

/tissue\_type="Embryonic Stem Cell"

/cell\_line="129.3 ES cells"

/lab\_host="DH10B"

/clone\_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long)"

/notes="vector: pCMV-SPORT6 (Invitrogen); Site 1: Salt; Site2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES cells were plated at density 3x103/cm2, on gelatin-coated plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGATCTAGTACCGAGCGCCCTTTTCTTTTCTTTT-3'] from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker Lf-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.8 kb. The library was constructed by Yulan Piao."

Query Match 25.7%; Score 380; DB 7; Length 481;

Best Local Similarity 88.0%; Pred. No. 5.9e-104;

Matches 426; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

QY 281 CGAAGTCAGAAGTCCTTGTAGTGTGGTCACTTTGTGTAAGTCAGGTGTAAGAGAGAA 340

Db 1 CGAAGTCAGAAGCTTGTGGCTGTGGTCACTTCCTGCTGAAGTCAGGTGCTTGAAGAGAA 60

QY 341 AGCAACCGGGGACATCTATGCTATGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 400

Db 61 GCGCAGCGGGGACGCTATGCCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120

QY 401 GCAGGTTTCATTTTTCAG 460

Db 121 ACAGGTTTCATTTTTCAG 180

QY 461 CCCCCAATTACAGTATGCCTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 520

Db 181 CCCCCAGTTACAGTATGCCTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

QY 521 GCTGAG 580

Db 241 GCTGAG 300

QY 581 GATACAGTTTACCTAGCTAGCTGATTTTGGCTGTTTTCACAGGCTTTCATCTGATGGATA 640

Db 301 GATCAGTTTACCTAGCTAGCTGATTTTGGCTGTTTTCACAGGCTTTCATCTGATGGATA 360

QY 641 CGTGATCGAG 700

Db 361 TGTGATCGAG 420

QY 701 GGTGGATTTTGGATCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760

Db 421 GGTGGATTTTGGATCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477

QY 761 GATT 764

Db 478 CATT 481

RESULT 9

LOCUS CN678533

DEFINITION E0112C12-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long) Mus musculus cDNA clone NIA:E0112C12 IMAGE:30777539 5', mRNA sequence.

ACCESSION CN678533

VERSION CN678533.1 GI:47444984

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases 1 to 479)

AUTHORS Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., VanBuren, V., Falco, G., Martin, P.R., Staggs, C.A., Bassey, U.C., Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelsoe, J., Hide, W. and Ko, M.S.

TITLE Transcriptome analysis of mouse stem cells and early embryos

JOURNAL PLoS Biol. 1 (3), 410-419 (2003)

COMMENT Contact: Dawood B. Dudekula Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: E0112 row: C column: 12 Seq primer: M13 Reverse High quality sequence stop: 479

[illegible]



4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .449

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/clone\_lib="Mus musculus 129Sv/Ev"

#### FEATURES

source

#### ORIGIN

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Best Local Similarity 91.8%; Pred. NO. 8.6e-88;
Matches 345; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Db 6 CTCTCTCCCTCCCTCGTTCCACCTCAAGTCGACGATGACACTCCAAATTTTGATGAAC 65

QY 1162 CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGACGTGAGCCCTCAGGCTTCTCGG 1221
    |||||
Db 66 CAGAGAAGAAATTCGTGGGTTTCATCTCTCTGTGTGCCAGCTGAGCCCTCTGGGCTTCTCAG 125

QY 1222 GTGAAGAACTGCGGTTTGTGGGTTTTCGTACGAAGGACACGCGGATCTTGGTAGAT 1281
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Db 126 GCGAAGAGCTGCGGTTTGTGGGATTTTCGTACGAAGGACACGCGGATCTTGGTAGAT 185

QY 1282 CTGAGTCTGTGTGTGGGTTCTGAGCTCCCTCCCAAGACTAGCTCCATGGAAGAAAC 1341
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Db 186 CTGAGTCTGTGTGTGGGTTCTGAGCTCCCTCCCAAGACTAGCTCCATGGAAGAAAC 245

QY 1342 TTCTCATAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAGGTTATTTATTT 1401
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Db 246 TTCTCATAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAGGTTATTTATTT 305

QY 1402 CCGCAGCGGCTCTCTCTGCTCCAGGATCTCTCCGTCGATATATGCAAGGATCCG 1461
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Db 306 CCACAGCGGCTCTCTGCTCCAGGATCTCTCCGTCGATATATGCAAGGATCTG 365

QY 1462 CCGCGGCGCTGCTGCTG 1477
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Db 366 CCGCGGCGCTGCTGCTG 381
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RESULT 13  
CG501400  
LOCUS  
DEFINITION  
OST45250 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST45250,  
mRNA sequence.

CG501400  
VERSION  
CG501400.1 GI:37275069  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 450)

AUTHORS  
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
Piggott,J., Beltrando,Rio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,  
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
Sparks,M.J., Van Slighthorst,I., Vogel,P., Walke,W., Xu,N.,  
Zhu,Q., Person,C. and Sands,A.T.

TITLE  
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
Contact: Zambrowicz BP

OmiBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

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/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129Sv/Ev"

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/clone="OST45250"

/cell\_type="embryonic stem cell"

/clone\_lib="Mus musculus 129Sv/Ev"

#### FEATURES

source

#### ORIGIN

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Best Local Similarity 91.7%; Pred. NO. 3.5e-87;
Matches 343; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1108 CCCCCTTCGTTCCACCTCAAGTCGACGATGACACTCCAAATTTTGATGAACGAGA 1167
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Db 2 CCCCCTTCGTTCCACCTCAAGTCGACGATGACACTCCAAATTTTGATGAACGAGA 61

QY 1168 AGAATTCGTGGGTTTCATCTCTCCGTCGACGTGAGCCCTCAGGCTTCTCGGTTGAAG 1227
    |||||
Db 62 AGAATTCGTGGGTTTCATCTCTCTGTGTGCCAGCTGAGCCCTCGGCTTCTCAGGCGAAG 121

QY 1228 AACTGCGGTTTGTGGGTTTTCGTACGAAGGACATCGGGATCTTGGTAGATCTGAGT 1287
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Db 122 AGTGGCGTTTGTGGGATTTTCGTACGAAGGACATCGGGATCTTGGTAGATCTGAGT 181

QY 1288 CTGTTGTGTGGGTTCTGGACTCCCTCCCAAGACTAGCTCCATGGAAGAAACAACTTCTCA 1347
    |||||
Db 182 CTGTTGTGTGGGTTCTGGACTCCCTCCCAAGACTAGCTCCATGGAAGAAACAACTTCTCA 241

QY 1348 TCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAGGTTATTTATTTTCCGCGAG 1407
    |||||
Db 242 TCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAGGTTATTTATTTTCCGCGAG 301

QY 1408 CCGGCTCTCTCTCTGCTCCAGGATCTCTCCGTCGATATGATGCAAGGATCTCCGCGGG 1467
    |||||
Db 302 CCGGCTCTCTCTCTGCTCCAGGATCTCTCCGTCGATATGATGCAAGGATCTCCGCGGG 361

QY 1468 GCGGCTCTGCTGCTC 1481
    |||||
Db 362 GCGGCTCTGCTGCTC 375
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#### RESULT 14

CG652891

LOCUS

DEFINITION

OST417039 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST417039,  
mRNA sequence.

CG652891

VERSION

CG652891.1 GI:37476740

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 512)

AUTHORS

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
Piggott,J., Beltrando,Rio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,  
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
Sparks,M.J., Van Slighthorst,I., Vogel,P., Walke,W., Xu,N.,  
Zhu,Q., Person,C. and Sands,A.T.

TITLE

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 06:24:41 ; Search time 749.892 Seconds  
(without alignments)  
11691.196 Million cell updates/sec

Title: US-10-724-594-1\_COPY\_17\_1497

Perfect score: 1481

Sequence: 1 tcaaatatgagcgcggaat.....cccgggcgctgctggctc 1481

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1481	100.0	1515	10 AAD59938	Aad59938 Human kin
3	1481	100.0	1515	12 ADO40591	Ado40591 Human kin
4	1477.8	99.8	1765	10 ABZ68726	Abz68726 Nucleotid
5	1476.2	99.7	2086	6 AAD26454	Aad26454 Human kin
6	1471.8	99.4	1485	10 ABZ68725	Abz68725 Nucleotid
7	1388.2	93.7	1870	8 ADA05643	Ada05643 Human NOV
8	1388.2	93.7	5877	6 ABQ78871	Abq78871 Human kin
9	1388.2	93.7	6156	9 AAL55217	Aal55217 Human CRI
10	1388.2	93.7	6165	6 AAD78870	Aad78870 Human kin
11	1388.2	93.7	6185	9 AAL55214	Aal55214 Human CRI
12	1388.2	93.7	6298	6 AAD38864	Aad38864 Human kin
13	1388.2	93.7	8603	9 AAL55215	Aal55215 Human CRI
14	1385	93.5	1870	12 ADN62808	Adn62808 Human NOV
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18	1381.8	93.3	6574	13 ADQ89099	Adq89099 Human uro
19	1372	92.6	6159	4 AAS06701	Aas06701 Polynucle
20	1372	92.6	8656	12 ADJ96544	Adj96544 Human cit

21	1365.8	92.2	6189	6 ABS63436	Abbs63436 RHO/RAC-1
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23	1365.8	92.2	6189	12 ADN62806	Adn62806 Human NOV
24	1365.8	92.2	6201	6 ABS63435	Abbs63435 Human CDN
25	1365.8	92.2	6201	8 ADA05653	Ada05653 Human NOV
26	1365.8	92.2	6201	12 ADN62818	Adn62818 Human NOV
27	1143.6	77.2	2380	10 ABZ68776	Abz68776 Nucleotid
28	947.2	64.0	2162	8 ABX71191	Abx71191 Novel hum
29	945.4	63.8	957	11 ADN62729	Adn62729 Human cit
30	925	62.5	1048	5 AAS79753	Aas79753 DNA encod
31	744.8	50.3	1133	10 ADJ79946	Adj79946 Human kin
32	578.8	39.1	2896	5 ABV30132	Abv30132 Human pro
33	441.8	29.8	446	5 ABV15823	Abv15823 Human pro
34	434.4	29.3	485	5 ABV45624	Abv45624 Human pro
35	247.2	16.7	3835	8 ABT33346	Abt33346 NOVA DNA
36	247.2	16.7	3985	8 ABT33347	Abt33347 NOVA DNA
37	246.8	16.7	1530	6 AAD38845	Aad38845 Human kin
38	246.8	16.7	4698	12 ADP47966	Adp47966 Human MRC
39	246.8	16.7	4707	12 ADP95101	Adp95101 Human ser
40	246.8	16.7	4944	12 ADP95099	Adp95099 Human ser
41	246.8	16.7	5373	6 AAD30567	Aad30567 Human kin
42	246.8	16.7	5373	12 ADQ15093	Adq15093 Human can
43	246.8	16.7	5438	12 ADJ96545	Adj96545 Human d/s
44	246.8	16.7	5619	12 ADI40903	Adi40903 Human kin
45	246.8	16.7	5973	10 ADC99116	Adc99116 Human KPP

ALIGNMENTS

RESULT 1  
ACA61394  
ID ACA61394 standard; cDNA; 1515 BP.  
XX  
AC ACA61394;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE cDNA encoding novel human kinase.  
XX  
KW Human; ss; gene; gene therapy; kinase; antisense.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 5'UTR 1..6  
FT CDS /\*tag= a  
7..1500  
/\*tag= b  
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FT 3'UTR 1501..1515  
/\*tag= c  
XX  
US2003022340-A1.  
PN  
XX  
30-JAN-2003.  
PD  
XX  
PF 11-SEP-2002; 2002US-00238709.  
XX  
PR 13-MAR-2001; 2001US-00804471.  
XX  
PA (APPL-) APPLERA CORP.  
XX  
PI Webster M, Yan C, Di Francesco V, Beasley EM;  
XX  
DR WPI; 2003-438978/41.  
XX  
DR P-PSDB; ABU10126.  
XX  
PT New human kinase peptides useful as models or targets for the development  
PT of therapeutic agents that modulate kinase activity, for eliciting immune  
PT response, and in identifying compounds that modulate kinase activity or  
PT expression.  
XX

Claim 4; Fig 1; 207pp; English.

PS The invention relates to a novel isolated human kinase. The kinase  
 CC peptides and nucleic acids are useful as models for the development of  
 CC human therapeutic targets, in the identification of therapeutic proteins,  
 CC and serve as targets for the development of human therapeutic agents that  
 CC modulate kinase activity in cells and tissues that express the kinase.  
 CC The proteins can be used to raise or to elicit another immune response,  
 CC as a reagent in assays designed to determine the levels of the protein in  
 CC biological fluids, as markers for tissue in which the corresponding  
 CC protein is preferentially expressed, in the identification of modulators  
 CC of the peptides and in pharmacogenomic analysis. The nucleic acids are  
 CC useful as hybridisation probes, in constructing vectors, host cells or  
 CC transgenic animals expressing all or a part of the nucleic acid, for  
 CC monitoring the effectiveness of modulating compounds on the expression or  
 CC activity of the transporter gene in clinical trials or in treatment  
 CC regimen, in gene therapy and as antisense constructs to control  
 CC transporter gene expression in cells, tissue and organisms. The present  
 CC sequence represents a novel human kinase  
 XX

SQ Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

Query Match 100.0%; Score 1481; DB 8; Length 1515;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCAAAATGGAGCGCGGAATCCTTTGGATGCTGCTGGTGTGCTGAACCCATTGCCAACCGGG	60
Db	17	TCAAAATGGAGCGCGGAATCCTTTGGATGCTGCTGGTGTGCTGAACCCATTGCCAACCGGG	76
Qy	61	CCTCAGCGCTGAATCTGTTCTTCCAGGGGAAACACACCTTTTATGACTCAACAGCAGATGT	120
Db	77	CCTCAGCGCTGAATCTGTTCTTCCAGGGGAAACACACCTTTTATGACTCAACAGCAGATGT	136
Qy	121	CTCCTCTTTCCGAGAGAGGATATAGATCCCTCTTTGTTCTCTTTTGAAGAATGCAATG	180
Db	137	CTCCTCTTTCCGAGAGAGGATATAGATCCCTCTTTGTTCTCTTTTGAAGAATGCAATG	196
Qy	181	AGCTGCTCTGATGAAGATTAAGCAGTGAACCTTTGTCGAGAGTATTCGACACCA	240
Db	197	AGCTGCTCTGATGAAGATTAAGCAGTGAACCTTTGTCGAGAGTATTCGACACCA	256
Qy	241	TAGCTGAGTTACAGAGCTCCAGCCTTCGGCAAGGACTTCGAAGTCAGAGTCTTTGTAG	300
Db	257	TAGCTGAGTTACAGAGCTCCAGCCTTCGGCAAGGACTTCGAAGTCAGAGTCTTTGTAG	316
Qy	301	GTTGTGTCTATTGCTGAAGTGCAGGTGTAGAGAGAAAGCAACCGGGGACATCTATG	360
Db	317	GTTGTGTCTATTGCTGAAGTGCAGGTGTAGAGAGAAAGCAACCGGGGACATCTATG	376
Qy	361	CTATGAAGTGTAGAGAGAGGCTTTATTTGGCCAGGAGCAGGTTTCATTTTGTAGG	420
Db	377	CTATGAAGTGTAGAGAGAGGCTTTATTTGGCCAGGAGCAGGTTTCATTTTGTAGG	436
Qy	421	AAGAGCGGAACATATTATCTGAAGCAACAGCCCGTGGATCCCGCAATTAAGTATGCTT	480
Db	437	AAGAGCGGAACATATTATCTGAAGCAACAGCCCGTGGATCCCGCAATTAAGTATGCTT	496
Qy	481	TTCAGGCAAAATATCACTTTATCTGTCATGGAATATACGCTGGAGGGGACTTGTGT	540
Db	497	TTCAGGCAAAATATCACTTTATCTGTCATGGAATATACGCTGGAGGGGACTTGTGT	556
Qy	541	CACTTTGTAGATAGAGGACAGTTAGATGAACCTGTATACATGATTTTACCTAGCTG	600
Db	557	CACTTTGTAGATAGAGGACAGTTAGATGAACCTGTATACATGATTTTACCTAGCTG	616
Qy	601	AGCTGATTTTGGCTGTTACAGCGGTTTCACTGTATGGGATACGTCATCGAGACATCAAG	660
Db	617	AGCTGATTTTGGCTGTTACAGCGGTTTCACTGTATGGGATACGTCATCGAGACATCAAG	676
Qy	661	CTGAGAACATCTCGTTGACCGCAGCAGACATCAAGCTGGTGGATTTTGGATCTGCCG	720
Db	677	CTGAGAACATCTCGTTGACCGCAGCAGACATCAAGCTGGTGGATTTTGGATCTGCCG	736

Qy	721	CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCAGATACA	780
Db	737	CGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCAGATACA	796
Qy	781	TGGCTCTCTGAAGTCTGACTGTGATGAACGGGGATGGAAGGACCTACGGGCTGGACT	840
Db	797	TGGCTCTCTGAAGTCTGACTGTGATGAACGGGGATGGAAGGACCTACGGGCTGGACT	856
Qy	841	GTGACTTGGTGGTCACTGGGCGTGAATTCCTATGAGATGATTTATGGAGATCCCTTCG	900
Db	857	GTGACTTGGTGGTCACTGGGCGTGAATTCCTATGAGATGATTTATGGAGATCCCTTCG	916
Qy	901	CAGAGGACCTTCCGACAACTTCAATAACATATGAATTTCCAGCGGTTTTTGAAT	960
Db	917	CAGAGGACCTTCCGACAACTTCAATAACATATGAATTTCCAGCGGTTTTTGAAT	976
Qy	961	TTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATTTCAAGCTTGTGTGCG	1020
Db	977	TTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATTTCAAGCTTGTGTGCG	1036
Qy	1021	GCAGAAAGAGAGACTGAAGTGTGAAGTCTTTGTGCGCATCTTTCTCTTAAATTTG	1080
Db	1037	GCAGAAAGAGAGACTGAAGTGTGAAGTCTTTGTGCGCATCTTTCTCTTAAATTTG	1096
Qy	1081	ACTGGAAACATTCGTAACTCTCTCCCGCTTCTGTTCCACCTCAAGTCCGACATG	1140
Db	1097	ACTGGAAACATTCGTAACTCTCTCCCGCTTCTGTTCCACCTCAAGTCCGACATG	1156
Qy	1141	ACACCTCCAAATTTGATGAACAGAGAAATTCGTGGGTTTCATCTCTCGTGCAGC	1200
Db	1157	ACACCTCCAAATTTGATGAACAGAGAAATTCGTGGGTTTCATCTCTCGTGCAGC	1216
Qy	1201	TGAGCCCTCAGCTTCTCGGGTGAAGAACTGCGCGTTTGTGGGTTTTCGTACAGCAAG	1260
Db	1217	TGAGCCCTCAGCTTCTCGGGTGAAGAACTGCGCGTTTGTGGGTTTTCGTACAGCAAG	1276
Qy	1261	CAGTGGGATCTTGTGTAGATCTGAGTCTGTGTGTCGGGCTTGGACTCCCTGCCAAG	1320
Db	1277	CAGTGGGATCTTGTGTAGATCTGAGTCTGTGTGTCGGGCTTGGACTCCCTGCCAAG	1336
Qy	1321	CTAGCTCCATGAAAGAAACTTCTCATCAAAAGCAAGAGCTTACAGACTCTCAGGACA	1380
Db	1337	CTAGCTCCATGAAAGAAACTTCTCATCAAAAGCAAGAGCTTACAGACTCTCAGGACA	1396
Qy	1381	AGTGTCAAGGATTTATTTCCGACGCGGCTCTCTTCTTCTCCAGATCTCTCCCT	1440
Db	1397	AGTGTCAAGGATTTATTTCCGACGCGGCTCTCTTCTTCTCCAGATCTCTCCCT	1456
Qy	1441	CGGTATATCCCAAGGATCCGCCCGGGCGCTGCTGGCTC	1481
Db	1457	CGGTATATCCCAAGGATCCGCCCGGGCGCTGCTGGCTC	1497

RESULT 2

AAD59938

ID AAD59938 standard; cDNA; 1515 BP.

XX AAD59938;

AC AAD59938;

XX 18-DEC-2003 (first entry)

DT 18-DEC-2003 (first entry)

XX Human kinase cDNA.

DE Human kinase cDNA.

XX Human; kinase protein; diagnostic; therapeutic; immune response;

KW pharmacogenomic; tissue typing; gene therapy; chromosome 12; transgenic;

KW gene; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key

5'UTR

FT

FT

FT

FT

FT

FT

FT

FT

FT

Location/Qualifiers

1..6

/\*tag= a



Db 1397 AGTGTCAAGGATATTATTTCCGACGCGGCTCTTCTCTGCTCCAGGATCCTCCCGT 1456

Qy 1441 CCCTATATGCCAAGGATTCGCGCGGGGCGCTCTCGGCTC 1481  
|||||  
Db 1457 CCCTATATGCCAAGGATTCGCGCGGGGCGCTCTCGGCTC 1497

RESULT 3  
ADO40591  
ID ADO40591 standard; cDNA; 1515 BP.  
XX AC  
XX ADO40591;  
XX 29-JUL-2004 (first entry)  
XX Human kinase cDNA.  
XX DE  
XX Kinase; rho/rac-interacting citron kinase; drug screening;  
XX KW kinase related disorder; human; chromosome 12; gene; ss.  
XX KW  
XX OS Homo sapiens.  
XX XX

Key Location/Qualifiers  
FH 1..6  
FT 5'UTR /tag= a  
FT 7..1500  
FT CDS /tag= b  
FT /product= "Human kinase protein"  
FT 1501..1515  
FT /tag= c

US2004091993-A1.  
XX PN  
XX 13-MAY-2004.  
XX PD  
XX 02-DEC-2003; 2003US-00724594.  
XX PF  
XX 13-MAR-2001; 2001US-00804471.  
XX PR  
XX 11-SEP-2002; 2002US-00238709.  
XX XX  
XX (APPL-) APPLERA CORP.  
XX XX  
XX Webster M, Yan C, Di Francesco V, Beasley EM;  
XX XX  
XX WPI: 2004-374957/35.  
XX DR P-PSDB; ADO40592.  
XX DR

New isolated human kinase proteins and nucleic acids, useful for developing human therapeutic targets, identifying therapeutic proteins or serve as targets for the development of human therapeutic agents that modulate kinase activity.

XX Claim 4; SEQ ID NO 1; 207pp; English.  
XX XX

The present invention provides a kinase polypeptide and its encoding polynucleotide. The polypeptide and polynucleotide of the invention are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The invention is also useful for biological assays related to kinases, in drug screening assays, for treating disorders characterized by an absence of inappropriate and unwanted expression of the protein. The present sequence is human kinase cDNA. The human kinase gene is located on chromosome 12.

XX CC  
XX Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;  
XX CC

Query Match  
Best Local Similarity 100.0%; Score 1481; DB 12; Length 1515;  
Matches 1481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAATATGAGCGCGGAATCCTTTTGGATCGTGTGCTGAACCCATTGCCAACCGGG 60  
|||||

Db 17 TCAATATGAGCGCGGAATCCTTTTGGATCGTGTGCTGAACCCATTGCCAACCGGG 76

Qy 61 CTTCAGGCTGAATCTGTCTTCACAGGGGAAACACCTTTATGACTCAACAGCAGATGT 120  
|||||  
Db 77 CTTCAGGCTGAATCTGTCTTCACAGGGGAAACACCTTTATGACTCAACAGCAGATGT 136  
|||||

Qy 121 CTCCTCTCTCCGAGAGGGATATTAGATGCCCTCTCTTGTCTCTTTGAAGATGCGATC 180  
|||||  
Db 137 CTCCTCTCTCCGAGAGGGATATTAGATGCCCTCTCTTGTCTCTTTGAAGATGCGATC 196  
|||||

Qy 181 AGCTGCTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCCGGAAGTATTCGACACCA 240  
|||||  
Db 197 AGCTGCTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCCGGAAGTATTCGACACCA 256  
|||||

Qy 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAAGTCAGAAGTCTGTAG 300  
|||||  
Db 257 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAAGTCAGAAGTCTGTAG 316  
|||||

Qy 301 GTTGTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 360  
|||||  
Db 317 GTTGTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 376  
|||||

Qy 361 CTATGAAGTGAAGAAAGAGGCTTTATTTGGCCCGAGGAGCAGGTTTCATTTTTGAGG 420  
|||||  
Db 377 CTATGAAGTGAAGAAAGAGGCTTTATTTGGCCCGAGGAGCAGGTTTCATTTTTGAGG 436  
|||||

Qy 421 AAGAGCGGAACATATTATCTCGAAGCACAAAGCCCGTGGATCCCCCAATTTACAGTATGCCT 480  
|||||  
Db 437 AAGAGCGGAACATATTATCTCGAAGCACAAAGCCCGTGGATCCCCCAATTTACAGTATGCCT 496  
|||||

Qy 481 TTCAGGACAAAATCACTTTTCTGTCATGAATATCAGCTGCTGAGGGGACTTCCTGT 540  
|||||  
Db 497 TTCAGGACAAAATCACTTTTCTGTCATGAATATCAGCTGCTGAGGGGACTTCCTGT 556  
|||||

Qy 541 CACTTTTGAATAGATATGAGGACCACTTAGATGAAAACCTGTATACAGTTTACCTAGCTG 600  
|||||  
Db 557 CACTTTTGAATAGATATGAGGACCACTTAGATGAAAACCTGTATACAGTTTACCTAGCTG 616  
|||||

Qy 601 AGCTGATTTGGCTGTTTCAAGGTTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660  
|||||  
Db 617 AGCTGATTTGGCTGTTTCAAGGTTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 676  
|||||

Qy 661 CTGAGAAATCTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720  
|||||  
Db 677 CTGAGAAATCTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 736  
|||||

Qy 721 CGAAATGAATTCAAACAAAGATGGTGAATGCCAAACTCCCGATTTGGGACCCAGATTACA 780  
|||||  
Db 737 CGAAATGAATTCAAACAAAGATGGTGAATGCCAAACTCCCGATTTGGGACCCAGATTACA 796  
|||||

Qy 781 TGGCTCTCTGAGTCTGACTGTGATGAACGGGGATGGAAGGCACCTACGGCCTGGACT 840  
|||||  
Db 797 TGGCTCTCTGAGTCTGACTGTGATGAACGGGGATGGAAGGCACCTACGGCCTGGACT 856  
|||||

Qy 841 GTGACTGTGGTTCAGTGGGCGTGAATGCTTATGAGATGATTTATGGAGATCCCCCTTCG 900  
|||||  
Db 857 GTGACTGTGGTTCAGTGGGCGTGAATGCTTATGAGATGATTTATGGAGATCCCCCTTCG 916  
|||||

Qy 901 CAGAGGAACTCTGCGCAGAACTTCAATAACATTAATGAATTTCCAGCGGTTTTGAAAT 960  
|||||  
Db 917 CAGAGGAACTCTGCGCAGAACTTCAATAACATTAATGAATTTCCAGCGGTTTTGAAAT 976  
|||||

Qy 961 TTCCAGATGACCCCAAGTGACAGTGAACGGGGATGGAAGGCACCTACGGCCTGGACT 1020  
|||||  
Db 977 TTCCAGATGACCCCAAGTGACAGTGAACGGGGATGGAAGGCACCTACGGCCTGGACT 1036  
|||||

Qy 1021 GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTTTTCTTCTTCTTAAATG 1080  
|||||  
Db 1037 GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTTTTCTTCTTAAATG 1096  
|||||

Qy 1081 ACTGGAACAAATTCGTAACTCTCTCCCTTCCTTCCTCCACCTCAAGTCCGAGATG 1140  
|||||  
Db 1097 ACTGGAACAAATTCGTAACTCTCTCCCTTCCTTCCTCCACCTCAAGTCCGAGATG 1156  
|||||

QY 1141 ACACCTCCAAATTTTGATGAACACGAGAGAAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1200  
DB 1157 ACACCTCCAAATTTTGATGAACACGAGAGAAATTCGTGGGTTTCATCCTCTCCGTGCCAGC 1216  
QY 1201 TGAGCCCTCAGGCTTCCTGGGTGAAGAACTGCGGTTTGGGGTTTTCGTACAGCAAGG 1260  
DB 1217 TGAGCCCTCAGGCTTCCTGGGTGAAGAACTGCGGTTTGGGGTTTTCGTACAGCAAGG 1276  
QY 1261 CACTGGGGATTTCTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCTCCGCAAGA 1320  
DB 1277 CACTGGGGATTTCTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCTCCGCAAGA 1336  
QY 1321 CTAGCTCCATGGAAGAAACTTTCTCATCAAAAGCAAGAGCTACAGACTCTCAGGACA 1380  
DB 1337 CTAGCTCCATGGAAGAAACTTTCTCATCAAAAGCAAGAGCTACAGACTCTCAGGACA 1396  
QY 1381 AGTGTCAAGAGTATTATTTCGCGAGCCGCGCTCTCTTCTGCTCAGGATCTCCCGT 1440  
DB 1397 AGTGTCAAGAGTATTATTTCGCGAGCCGCGCTCTCTTCTGCTCAGGATCTCCCGT 1456  
QY 1441 CCGTATATGCAAGAGGATCCGCGCGCGCGCTGCTGCTC 1481  
DB 1457 CCGTATATGCAAGAGGATCCGCGCGCGCGCTGCTGCTC 1497

## RESULT 4

ABZ68726  
ID ABZ68726 standard; DNA; 1765 BP.  
AC ABZ68726;  
XX  
DT 16-MAY-2003 (first entry)  
XX  
DE Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.  
XX  
KW Human; citron rho/rac-interacting kinase-short kinase; obesity;  
KW chronic obstructive pulmonary disease; hypertension; diabetes;  
KW coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;  
KW gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;  
KW polycystic ovarian syndrome; fertility; depression; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..1494  
FT /\*tag= a  
FT /product= "citron rho/rac-interacting kinase-short  
FT kinase"  
XX  
PN W02003004629-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 01-JUL-2002; 2002WO-BF007229.  
XX  
PR 02-JUL-2001; 2001US-0301853P.  
PR 10-DEC-2001; 2001US-0337130P.  
PR 25-APR-2002; 2002US-0375015P.  
XX  
PA (PARB ) BAYER AG.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2003-221595/21.  
DR P-PSDB; ABP97687.  
XX  
PT New human citron rho/rac-interacting kinase-short kinase polypeptide and  
PT polynucleotide for preventing or treating diseases associated with the  
PT polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary  
PT disease.  
XX  
PS Claim 1; Fig 18; 145pp; English.

XX  
CC The present sequence encodes a human citron rho/rac-interacting kinase-  
CC short kinase polypeptide. The polynucleotide and polypeptide of the  
CC invention are useful in preventing, ameliorating, or treating disease  
CC associated with the polypeptide dysfunction. The expression vector of the  
CC reagent is useful in the preparation of a medicament for modulating the  
CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
CC disease, such as obesity or chronic obstructive pulmonary disease. These  
CC may also be used for treating obesity/ overweight-associated  
CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
CC apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced  
CC fertility, and depression  
XX  
SQ Sequence 1765 BP; 428 A; 430 C; 444 G; 463 T; 0 U; 0 Other;

Query Match 99.8%; Score 1477.8; DB 10; Length 1765;  
Best Local Similarity 99.9%; Pred. NO. 0;  
Matches 1479; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TCAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATTGCCAACCGGG 60  
DB 11 TCAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATTGCCAACCGGG 70  
QY 61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATGACTCAACAGCAGATGT 120  
DB 71 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATGACTCAACAGCAGATGT 130  
QY 121 CTCCTCTTCCGAGAGGAGATATTAGATGCTCTTTGTTCTCTTTGTTCTTTGAAGATGCGATC 180  
DB 131 CTCCTCTTCCGAGAGGAGATATTAGATGCTCTTTGTTCTCTTTGTTCTTTGAAGATGCGATC 190  
QY 181 AGCTCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCGCGAAGTATTTCGACACCA 240  
DB 191 AGCTCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCGCGAAGTATTTCGACACCA 250  
QY 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGCGAAGGACTTCGAAAGTCAGAAAGTCTTGTAG 300  
DB 251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGCGAAGGACTTCGAAAGTCAGAAAGTCTTGTAG 310  
QY 301 GTTGTGTCACCTTTGCTGAAGTGCAGTGGTAAAGAGAAAGCAACCGGGGACATCTATG 360  
DB 311 GTTGTGTCACCTTTGCTGAAGTGCAGTGGTAAAGAGAAAGCAACCGGGGACATCTATG 370  
QY 361 CTATGAAAGTGAAGAAGAGAGGCTTTATTCGCGCAGAGCAGGTTTCATTTTTTGGAG 420  
DB 371 CTATGAAAGTGAAGAAGAGAGGCTTTATTCGCGCAGAGCAGGTTTCATTTTTTGGAG 430  
QY 421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCTT 480  
DB 431 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCTT 490  
QY 481 TTCAGGACAAAATACCTTTTATCTGGTCAATGAATATCAGCCTGGAGGGGACTTGTGT 540  
DB 491 TTCAGGACAAAATACCTTTTATCTGGTCAATGAATATCAGCCTGGAGGGGACTTGTGT 550  
QY 541 CACTTTTGAATAGATATGAGGACCACTAGATGABAAACCTGTATACAGTTTACCTAGCTG 600  
DB 551 CACTTTTGAATAGATATGAGGACCACTAGATGABAAACCTGTATACAGTTTACCTAGCTG 610  
QY 601 AGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660  
DB 611 AGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670  
QY 661 CTGAGAAATTTCTGTTGACCGCAGCAGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720  
DB 671 CTGAGAAATTTCTGTTGACCGCAGCAGCAGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730  
QY 721 CGAAATGATTCMAACAGATGGTCAATGCCAACTCCGATTGGGACCCAGATTACA 780  
DB 731 CGAAATGATTCMAACAGATGGTCAATGCCAACTCCGATTGGGACCCAGATTACA 790  
QY 781 TGGCTCTCGAAGTGTCTGACTGTGATGAACGGGGATGGAAGGCAACCTACGGCTGGACT 840



121 CTCTCTTTCCGAGAGGAGATATTAGATGCCCTCTTTGTTCTTTGTTGAAGAAATGCAGTC 180  
144 CTCTCTTTCCGAGAGGAGATATTAGATGCCCTCTTTGTTCTTTGTTGAAGAAATGCAGTC 203  
181 AGCTGCTCTGATGAGATTAAGCAGTGTAGCAACTTTGTCGGAGAGTATTCCGACACCA 240  
204 AGCTGCTCTGATGAGATTAAGCAGTGTAGCAACTTTGTCGGAGAGTATTCCGACACCA 263  
241 TAGCTGAGTTTACAGGAGCTCCAGCCTTTCCGCAAGGACTTTGGAAGTCAGAAAGTCTTGATG 300  
264 TAGCTGAGTTTACAGGAGCTCCAGCCTTTCCGCAAGGACTTTGGAAGTCAGAAAGTCTTGATG 323  
301 GTTGTGCTACTTTGCTGTAAGTGTAGTGTATAGAGAGAAAGCAACCGGGGACATCTATG 360  
324 GTTGTGCTACTTTGCTGTAAGTGTAGTGTATAGAGAGAAAGCAACCGGGGACATCTATG 383  
361 CTATGAAAGTGATGAAAGAAAGGCTTTATTTGCCCCAGGAGAGTTCATTTTTTTGAGG 420  
384 CTATGAAAGTGATGAAAGAAAGGCTTTATTTGCCCCAGGAGAGTTCATTTTTTTGAGG 443  
421 AAGAGGGGAAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTACAGTATGCCT 480  
444 AAGAGGGGAAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTACAGTATGCCT 503  
481 TTGAGGACAAAATACACTTTATCTGCTCATGGAATATACAGCTGTGAGGGGACTTGTCTGT 540  
504 TTGAGGACAAAATACACTTTATCTGCTCATGGAATATACAGCTGTGAGGGGACTTGTCTGT 563  
541 CACTTTGATAGATAGAGGACAGTATAGATGAAACCTGATACAGTATTTTACCTAGCTG 600  
564 CACTTTGATAGATAGAGGACAGTATAGATGAAACCTGATACAGTATTTTACCTAGCTG 623  
601 AGCTGATTTTGGCTGTTTACAGCGTTTATCTGATGGGATACGTGATCGAGACATCAAGC 660  
624 AGCTGATTTTGGCTGTTTACAGCGTTTATCTGATGGGATACGTGATCGAGACATCAAGC 683  
661 CTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGTGGATTTTGGATCTGCCG 720  
684 CTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGTGGATTTTGGATCTGCCG 743  
721 CGAAATGAATTTCAACAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
744 CGAAATGAATTTCAACAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 803  
781 TGCTCTCTGAGTCTGACTGTGATGAAACCGGATGGAAGGACCTACCGGCTGACT 840  
804 TGCTCTCTGAGTCTGACTGTGATGAAACCGGATGGAAGGACCTACCGGCTGACT 863  
841 GTGACTGTGTTGAGTGGGCGTGAATTCCTATGAGATGATTTATGGGAGATCCCCCTTGG 900  
864 GTGACTGTGTTGAGTGGGCGTGAATTCCTATGAGATGATTTATGGGAGATCCCCCTTGG 923  
901 CAGAGGAACTTCTGCGAGAACCTTCAATTAACATTAATTAATTAATTAATTAATTAATTAAT 960  
924 CAGAGGAACTTCTGCGAGAACCTTCAATTAACATTAATTAATTAATTAATTAATTAATTAAT 983  
961 TTCCAGATGATCCCAAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
984 TTCCAGATGATCCCAAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1043  
1021 GCCAGAAAGAGAGACTGAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGG 1080  
1044 GCCAGAAAGAGAGACTGAAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGG 1103  
1081 ACTGGAACAAACATTTGTAACCTTCTCCCTTCTGTTCCACCTTCAAGTCCGAGATG 1140  
1104 ACTGGAACAAACATTTGTAACCTTCTCCCTTCTGTTCCACCTTCAAGTCCGAGATG 1163  
1141 ACACCTCCAAATTTTGTATGAAACAGAGAAATTTGTTGGGTTTCTCTCTCGTGGCCAGC 1200  
1164 ACACCTCCAAATTTTGTATGAAACAGAGAAATTTGTTGGGTTTCTCTCTCGTGGCCAGC 1223  
1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTCGTACAGCAAGG 1260

1224 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTCGTACAGCAAGG 1283  
1261 CACTGGGGATTTCTTGTAGATCTGAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320  
1284 CACTGGGGATTTCTTGTAGATCTGAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1343  
1321 CTAGCTCCATGGAAGAAAGAACTTTCTCATCAAAAGCAAGAGCTTCAAGACTCTCAGGACA 1380  
1344 CTAGCTCCATGGAAGAAAGAACTTTCTCATCAAAAGCAAGAGCTTCAAGACTCTCAGGACA 1403  
1381 AGTGTACAAAGTATTTATTTTCCGAGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440  
1404 AGTGTACAAAGTATTTATTTTCCGAGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1463  
1441 CGTATATATCCAAAGGATCCGCCGGGCGCTGCTGGGCTC 1481  
1464 CGTATATATCCAAAGGATCCGCCGGGCGCTGCTGGGCTC 1504

RESULT 6  
ABZ68725  
ID ABZ68725 standard; DNA; 1485 BP.  
XX  
AC ABZ68725;  
XX  
DT 16-MAY-2003 (first entry)  
XX  
DE Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.  
XX  
KW Human; citron rho/rac-interacting kinase-short kinase; obesity;  
XX chronic obstructive pulmonary disease; hypertension; diabetes;  
XX coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;  
XX gout; osteoarthritis; sleep apnea; cancer; thrombotic disease;  
XX polycystic ovarian syndrome; fertility; depression; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key  
CDS 1..1485  
FT /\*tag= a  
FT /partial  
FT /product= "citron rho/rac-interacting kinase-short  
FT kinase"  
XX  
XX WO2003004629-A2.  
XX  
XX 16-JAN-2003.  
XX  
XX 01-JUL-2002; 2002WO-BP007229.  
XX  
XX 02-JUL-2001; 2001US-0301853P.  
XX 10-DEC-2001; 2001US-0337130P.  
XX 25-APR-2002; 2002US-0375015P.  
XX  
XX (FARB ) BAYER AG.  
XX  
XX Zhu Z;  
XX  
XX WPI; 2003-221595/21.  
XX P-PSDB; ABP97681.  
XX  
XX New human citron rho/rac-interacting kinase-short kinase polypeptide and  
XX polynucleotide for preventing or treating diseases associated with the  
XX polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary  
XX disease.  
XX  
XX Claim 1; Fig 1; 145pp; English.  
XX  
XX The present sequence encodes a human citron rho/rac-interacting kinase-  
XX short kinase polypeptide. The polynucleotide and polypeptide of the  
XX invention are useful in preventing, ameliorating, or treating diseases  
XX associated with the polypeptide dysfunction. The expression vector or the



CC reagent is useful in the preparation of a medicament for modulating the  
CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
CC disease, such as obesity or chronic obstructive pulmonary disease. These  
CC may also be used for treating obesity/ overweight-associated  
CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
CC apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced  
CC fertility, and depression  
XX  
SQ Sequence 1485 BP; 373 A; 353 C; 372 G; 387 T; 0 U; 0 Other;

Query Match 99.4%; Score 1471.8; DB 10; Length 1485;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1473; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCAAATATGGAGCGCGGAATCTTTGGATGCTGTGCTGTAACCACTTGAAGTTCAGAGATGT 120  
Db 11 TCAAATATGGAGCGCGGAATCTTTGGATGCTGTGCTGTAACCACTTGAAGTTCAGAGATGT 130

Qy 61 CCTCAGGCTGAATCTCTTCCAGGGAACCACTTTATGACTCAACAGCAGATGT 120  
Db 71 CCTCAGGCTGAATCTCTTCCAGGGAACCACTTTATGACTCAACAGCAGATGT 130

Qy 121 CTCCTCTTCCGAGAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGATGCAATC 180  
Db 131 CTCCTCTTCCGAGAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGATGCAATC 190

Qy 181 AGCTGCTGTGATGAAGATTAAGCAGTGAACAACTTTGTCGGGAAGTATTCGACACCA 240  
Db 191 AGCTGCTGTGATGAAGATTAAGCAGTGAACAACTTTGTCGGGAAGTATTCGACACCA 250

Qy 241 TAGCTGAGTTACAGAGCTCCAGCTTCCGCAAGGACTTCGAGTCAGAGTCTGTAG 300  
Db 251 TAGCTGAGTTACAGAGCTCCAGCTTCCGCAAGGACTTCGAGTCAGAGTCTGTAG 310

Qy 301 GTTGTGTCATTTTGTGTAAGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 360  
Db 311 GTTGTGTCATTTTGTGTAAGTGCAGGTGTAAGAGAGAAAGCAACCGGGGACATCTATG 370

Qy 361 CTATGAAGTGAAGAGAGAGCTTTTATGCGCCAGAGAGAGGTTTCAATTTTGTAGG 420  
Db 371 CTATGAAGTGAAGAGAGAGCTTTTATGCGCCAGAGAGAGGTTTCAATTTTGTAGG 430

Qy 421 AAGAGCGGAACATATATCTGAAGCACAAGCCCGTGTGATCCCAATTAAGTATGSCCT 480  
Db 431 AAGAGCGGAACATATATCTGAAGCACAAGCCCGTGTGATCCCAATTAAGTATGSCCT 490

Qy 481 TTCAGGACAAAATCACCTTTATCTGTCATGGAATATCAGCTGAGGGGACTTGTGT 540  
Db 491 TTCAGGACAAAATCACCTTTATCTGTCATGGAATATCAGCTGAGGGGACTTGTGT 550

Qy 541 CACTTTGATAGATAGAGACCAAGTTAGATGAACACCTGTATACAGTTTACCTAGCTG 600  
Db 551 CACTTTGATAGATAGAGACCAAGTTAGATGAACACCTGTATACAGTTTACCTAGCTG 610

Qy 601 AGCTGATTTTGGCTGTTTCAAGAGCTTCACTGTGATGATACAGTGCATCGAGACATCAAG 660  
Db 611 AGCTGATTTTGGCTGTTTCAAGAGCTTCACTGTGATGATACAGTGCATCGAGACATCAAG 670

Qy 661 CTGAGAACATTTCTGTTGACCGCAGGACACATCAAGCTGTTGGAATTTTGGATCTGCCG 720  
Db 671 CTGAGAACATTTCTGTTGACCGCAGGACACATCAAGCTGTTGGAATTTTGGATCTGCCG 730

Qy 721 CGAAATGAATTCACAAAGATGGTGAATGCCAACTCCCGATTTGGACCCAGATATCA 780  
Db 731 CGAAATGAATTCACAAAGATGGTGAATGCCAACTCCCGATTTGGACCCAGATATCA 790

Qy 781 TGGCTCTGAAGTCTGACTGTGATGAACCGGGATGAAAGGCACTACGGCTTGGACT 840  
Db 791 TGGCTCTGAAGTCTGACTGTGATGAACCGGGATGAAAGGCACTACGGCTTGGACT 850

Qy 841 GTGACTGGTGCAGTGGGCGTGAATTCCTATGAGATGATTTATGGAGATCCCTCTTCG 900

Db 851 GTGACTGGTGCAGTGGGCGTGAATTCCTATGAGATGATTTATGGAGATCCCTCTTCG 910  
Qy 901 CAGAGGGAACCTCTGCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAT 960  
Db 911 CAGAGGGAACCTCTGCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTTGAAT 970

Qy 961 TTCAGATGACCCCAAGTGCAGTGCAGTCTTCTGATCTGATTTCAAGCTTCTGTGGC 1020  
Db 971 TTCAGATGACCCCAAGTGCAGTGCAGTCTTCTGATCTGATTTCAAGCTTCTGTGGC 1030

Qy 1021 GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTTTCTCTCTAAAATTG 1080  
Db 1031 GCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTTTCTCTCTAAAATTG 1090

Qy 1081 ACTGGAACAACTTCCTCTCCCTTCCTTCCTCCCTTCCTTCCTCCCTCAAGTCTGAGATG 1140  
Db 1091 ACTGGAACAACTTCCTCTCCCTTCCTTCCTCCCTTCCTTCCTCCCTCAAGTCTGAGATG 1150

Qy 1141 ACACCTCCCAATTTTGAAGTGCAGAACAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1200  
Db 1151 ACACCTCCCAATTTTGAAGTGCAGAACAAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1210

Qy 1201 TGAGCCCTCAGGCTTCTCGGCTGAAGAACTGCCGTTTGTGGGGTTTTTGTACAGCAAGG 1260  
Db 1211 TGAGCCCTCAGGCTTCTCGGCTGAAGAACTGCCGTTTGTGGGGTTTTTGTACAGCAAGG 1270

Qy 1261 CACTGGGATTTCTGTGATGATCTGATCTGTTGTGTGTGGGTTTGGACTCTCCCTGCCAAGA 1320  
Db 1271 CACTGGGATTTCTGTGATGATCTGATCTGTTGTGTGTGGGTTTGGACTCTCCCTGCCAAGA 1330

Qy 1321 CTAGCTCCATGGAAGAAACCTTCTCATCAAGCAAGAGCTTACAAAGACTCTCAGGACA 1380  
Db 1331 CTAGCTCCATGGAAGAAACCTTCTCATCAAGCAAGAGCTTACAAAGACTCTCAGGACA 1390

Qy 1381 AGTGTCAAGGTATTTATTTCCGACGCGGCTCTCTCTTGTCTCAGGATCTCCCGT 1440  
Db 1391 AGTGTCAAGGTATTTATTTCCGACGCGGCTCTCTCTTGTCTCAGGATCTCCCGT 1450

Qy 1441 CGGTATATGCCAAGGATCGCCCGGGCGGCTGC 1475  
Db 1451 CGGTATATGCCAAGGATCGCCCGGGCGGCTGC 1485

RESULT 7  
ADRA05643  
ID ADA05643 standard; cDNA; 1870 BP.  
XX  
AC ADA05643;  
XX AC  
XX AC  
DT 06-NOV-2003 (first entry)  
XX  
DE Human NOV1b encoding cDNA SEQ ID NO:3.  
XX  
XX human; NOV1; antidiabetic; anorectic; antibacterial; virucide;  
KW immunomodulator; cytostatic; nootropic; neuroprotective;  
KW antiparkinsonian; antilipemic; gene therapy; human disease;  
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;  
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
KW immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 2..1870  
FT /tag= a  
FT /product= "NOV1b"  
XX  
XX WO2003029424-A2.  
XX  
XX  
PD 10-APR-2003.  
XX  
XX 02-OCT-2002; 2002WO-US031373.  
XX  
XX









QY	301	GTGTGGTCACTTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGACACTCTATG	360
DB	311	GTGTGGTCACTTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGACACTCTATG	370
QY	361	CTATGAAAGTCAATGAAGAAGAGCGCTTTATTTGGCCCGAGGACAGGTTTCATTTTTCGAG	420
DB	371	CTATGAAAGTCAATGAAGAAGAGCGCTTTATTTGGCCCGAGGACAGGTTTCATTTTTCGAG	430
QY	421	AAGAGCGGAACATATTTATCTCGAAGCAACAAGCCCGTGTATCCGCCAAATTACAGTATGCCT	480
DB	431	AAGAGCGGAACATATTTATCTCGAAGCAACAAGCCCGTGTATCCGCCAAATTACAGTATGCCT	490
QY	481	TTCAGGACAAAATCACCTTTATCTGTGCATGGAAATATCAGCCTGGAGGGACCTGTCTGT	540
DB	491	TTCAGGACAAAATCACCTTTATCTGTGCATGGAAATATCAGCCTGGAGGGACCTGTCTGT	550
QY	541	CACTTTTGAATAGATATCAGGACCAAGTTTGTAGTGAATAAACCCTCATACAGTTTTTACCTAGCTG	600
DB	551	CACTTTTGAATAGATATCAGGACCAAGTTTGTAGTGAATAAACCCTCATACAGTTTTTACCTAGCTG	610
QY	601	AGCTGATTTGGCTGTTTCACAGCGTTTCATCTGTATGGGATACGTGCATCGAGACATCAAGC	660
DB	611	AGCTGATTTGGCTGTTTCACAGCGTTTCATCTGTATGGGATACGTGCATCGAGACATCAAGC	670
QY	661	CTGAGAACATTTCTCGTTGACCGGACAGGACACATCAAGCTGGTGGATTTTGGATCTGCGG	720
DB	671	CTGAGAACATTTCTCGTTGACCGGACAGGACACATCAAGCTGGTGGATTTTGGATCTGCGG	730
QY	721	CGAAAAATGAATTCAAAAAAGATGTTGAATGCGCAAACTCCCGATTTGGAGCCCAAGATTACA	780
DB	731	CGAAAAATGAATTCAAAAAAGATGTTGAATGCGCAAACTCCCGATTTGGAGCCCAAGATTACA	790
QY	781	TGGCTCTCTGAAGTCTGACTGTGATGAACGGGGATGGAAGGACACTTACGGCCTGGACT	840
DB	791	TGGCTCTCTGAAGTCTGACTGTGATGAACGGGGATGGAAGGACACTTACGGCCTGGACT	850
QY	841	GTGACTGGTGTGACTGGGCGTGATTCGCTATGAGATGATTTATGGGAGATCTCCCTTCG	900
DB	851	GTGACTGGTGTGACTGGGCGTGATTCGCTATGAGATGATTTATGGGAGATCTCCCTTCG	910
QY	901	CAGAGGGAACTCTGCGCAGAACCTTCAATTAACATTTATGAATTTCCAGCGGTTTTTGAAT	960
DB	911	CAGAGGGAACTCTGCGCAGAACCTTCAATTAACATTTATGAATTTCCAGCGGTTTTTGAAT	970
QY	961	TTCCAGATGACCCCAAAGTAGAGAGTGAATTTCTTGATCTGATTTCAAAGCTTGTGTGCG	1020
DB	971	TTCCAGATGACCCCAAAGTAGAGAGTGAATTTCTTGATCTGATTTCAAAGCTTGTGTGCG	1030
QY	1021	GCCAGAAGAGAGACTGAAGTTTCAAGGTCTTTGCTGCCATCCTTTCTTCTCTTAAATTTG	1080
DB	1031	GCCAGAAGAGAGACTGAAGTTTCAAGGTCTTTGCTGCCATCCTTTCTTCTCTTAAATTTG	1090
QY	1081	ACTGGAACAACTTCGTAACTCTCTCCGCCCTTCGTTCCACCCCTCAAAGTCGACGATG	1140
DB	1091	ACTGGAACAACTTCGTAACTCTCTCCGCCCTTCGTTCCACCCCTCAAAGTCGACGATG	1150
QY	1141	ACACCTCCAAATTTTGATGAACAGAGAGAATTCGTGGGTTTCATCTCTCCGTCGACG	1200
DB	1151	ACACCTCCAAATTTTGATGAACAGAGAGAATTCGTGGGTTTCATCTCTCCGTCGACG	1210
QY	1201	TGAGCCCTCAGGCTCTCCGGTGAAGACTGGCGGTTTGTGGGGTTTTTCGTACAGCAAG	1260
DB	1211	TGAGCCCTCAGGCTCTCCGGTGAAGACTGGCGGTTTGTGGGGTTTTTCGTACAGCAAG	1270
QY	1261	CACCTGGGGATTTCTGGTAGATCTGAGTCTGTTGTGTCGGGTCTTGGACTCCCTCGCCAGA	1320
DB	1271	CACCTGGGGATTTCTGGTAGATCTGAGTCTGTTGTGTCGGGTCTTGGACTCCCTCGCCAGA	1330
QY	1321	CTAGCTCCATGGAAAAGAACTTCTCATAAAGCAAAGAGCTACAAGACTCTCAGGACA	1380
DB	1331	CTAGCTCCATGGAAAAGAACTTCTCATAAAGCAAAGAGCTACAAGACTCTCAGGACA	1390

QY	1381	AGTGTCAACAGGT	1393
DB	1391	AGTGTCAACAGAT	1403
RESULT 10			
ABQ78870			
ID	ABQ78870	standard; cDNA; 6165 BP.	
XX	AC	AC	
XX	ABQ78870;		
XX	10-OCT-2002	(first entry)	
XX	DE	Human kinase cDNA #1.	
XX	KW	Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;	
KW	KW	Citron rho-interacting kinase; gene therapy; mental disorder; cancer;	
KW	KW	gene; ss.	
XX	OS	Homo sapiens.	
XX	XX		
FH	Key	Location/Qualifiers	
FT	CDS	1. .6165	
FT	FT	/*tag= a	
FT	FT	/product= "Kinase"	
FT	FT	replace(5218,G)	
FT	FT	/*tag= b	
FT	FT	/standard_name= "Single nucleotide polymorphism"	
FT	FT	replace(6065,G)	
FT	FT	/*tag= b	
FT	FT	/standard_name= "Single nucleotide polymorphism"	
XX	XX		
PN	WO200259325-A2.		
XX	XX		
PD	01-AUG-2002.		
XX	XX		
PP	20-DEC-2001; 2001WO-US050497.		
XX	XX		
PR	27-DEC-2000; 2000US-0258335P.		
XX	XX	(LEXI-) LEXICON GENETICS INC.	
PA	XX		
XX	XX		
PI	Yu X, Miranda M, Friddle CJ;		
XX	XX		
DR	WPI; 2002-599796/64.		
DR	P-PSDB; ABB81927.		
XX	XX		
PT	Novel polynucleotide encoding human proteins that are structurally		
PT	similar to animal kinases, useful for drug screening, diagnosis, in ge		
PT	therapy of disorders and diseases e.g. cancer and pharmacogenomic		
PT	applications.		
XX	XX		
PS	Claim 1; Page 37-39; 50pp; English.		
XX	XX		
CC	The invention relates to a novel human protein that shares structural		
CC	similarity with animal kinases, including serine-threonine kinases,		
CC	particularly Citron rho-interacting kinases. The proteins of the		
CC	invention have nootropic and cytostatic activity. The polynucleotides		
CC	have a use in gene therapy. The encoded novel polypeptides are useful		
CC	generating antibodies, as reagents in diagnostic assays, for identifi		
CC	other cellular gene products related to NHP and as reagents in assays		
CC	screening for compounds that are useful in the treatment of mental,		
CC	biological or medical disorders and diseases including cancer. The		
CC	sequence encodes a novel human kinase of the invention		
XX	XX		
SQ	Sequence 6165 BP; 1735 A; 1550 C; 1679 G; 1201 T; 0 U; 0 Other;		

Qy 1 TCAAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGGTGAACCCATTGCCAACCGG

Db 11 TCAATAATGAGCGCGGATCTTTGGATGCTGGTCTGCTGAACCCATTCGACGCGGG 70  
QY 61 CTTCCAGGCTGAATCTGTCTTCCAGGGGAAACACACCTTTATGACTCAACACAGATGT 120  
Db 71 CTTCCAGGCTGAATCTGTCTTCCAGGGGAAACACACCTTTATGACTCAACACAGATGT 130  
QY 121 CTCCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTTTGTAAGAAATGCAGTC 180  
Db 131 CTCCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTTTGTAAGAAATGCAGTC 190  
QY 181 AGCTGCTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCCGGAAGTATTCGACACCA 240  
Db 191 AGCTGCTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCCGGAAGTATTCGACACCA 250  
QY 241 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAGGACTTCGAAAGTCAGAGTCTTTGTAG 300  
Db 251 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAGGACTTCGAAAGTCAGAGTCTTTGTAG 310  
QY 301 GTTGTGGTCACTTTGCTGAAGTCAGGTGTTAAGAGAGAAAGCAACCGGGACATCTATG 360  
Db 311 GTTGTGGTCACTTTGCTGAAGTCAGGTGTTAAGAGAGAAAGCAACCGGGACATCTATG 370  
QY 361 CTATGAAGTGAATGAAGAGAGGCTTTATTTGCCCGAGGAGCAGGTTTCATTTTTGAGG 420  
Db 371 CTATGAAGTGAATGAAGAGAGGCTTTATTTGCCCGAGGAGCAGGTTTCATTTTTGAGG 430  
QY 421 AAGAGCGGAACATATTATCTCGAAGCACAGCCGCTGGATCCCCCAATTTACAGTATGCCT 480  
Db 431 AAGAGCGGAACATATTATCTCGAAGCACAGCCGCTGGATCCCCCAATTTACAGTATGCCT 490  
QY 481 TTGAGGACAAAATTCACCTTTATCTGCTCATGGAATATCAGCTGGAGGGGACTTCTGT 540  
Db 491 TTGAGGACAAAATTCACCTTTATCTGCTCATGGAATATCAGCTGGAGGGGACTTCTGT 550  
QY 541 CACTTTTGAATAGATGAGGACAGTTAGATGAAACCTGTGATACAGTTTACCTAGCTG 600  
Db 551 CACTTTTGAATAGATGAGGACAGTTAGATGAAACCTGTGATACAGTTTACCTAGCTG 610  
QY 601 AGCTGATTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTCATCGAGACATCAAGC 660  
Db 611 AGCTGATTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTCATCGAGACATCAAGC 670  
QY 661 CTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720  
Db 671 CTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730  
QY 721 CGAAATGAATTCAAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCAGATTACA 780  
Db 731 CGAAATGAATTCAAACAGATGGTGAATGCCAAACTCCCGATTGGGACCCAGATTACA 790  
QY 781 TGGCTCTGAAGTCTGACTGTGATGAAACGGGATGGAAGGACCTACGGCTCGACT 840  
Db 791 TGGCTCTGAAGTCTGACTGTGATGAAACGGGATGGAAGGACCTACGGCTCGACT 850  
QY 841 GTCACTGGTGGTCAAGTGGGCGTGAATGCCCTATGAGATGATTTATGGAGATCCCCCTTCG 900  
Db 851 GTCACTGGTGGTCAAGTGGGCGTGAATGCCCTATGAGATGATTTATGGAGATCCCCCTTCG 910  
QY 901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTGAAAT 960  
Db 911 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGGTTTTGAAAT 970  
QY 961 TTCCAGATGACCCCAAGTCAAGTCAAGTCACTTTCTGATCTGATTCAGAGCTTTGTGGG 1020  
Db 971 TTCCAGATGACCCCAAGTCAAGTCAAGTCACTTTCTGATCTGATTCAGAGCTTTGTGGG 1030  
QY 1021 GCCAGAAAGAGAGACTGAAGTCTTTGAGGCTCTTTGCTGCCATCTTTCTCTAAATTTG 1080  
Db 1031 GCCAGAAAGAGAGACTGAAGTCTTTGAGGCTCTTTGCTGCCATCTTTCTCTAAATTTG 1090  
QY 1081 ACTGGGAACAACTTGGTAACTCTCTCCCTCCCTTCGTTCCCACTCAAGTCGACGATG 1140  
Db 1091 ACTGGGAACAACTTGGTAACTCTCTCCCTCCCTTCGTTCCCACTCAAGTCGACGATG 1150

QY 1141 ACACCTCCAAATTTGATGAACACAGAGAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1200  
Db 1151 ACACCTCCAAATTTGATGAACACAGAGAATTCGTGGGTTTCATCTCTCCGTGCCAGC 1210  
QY 1201 TGAGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCGCGTTTGTGGGTTTTCGTACAGCAAG 1260  
Db 1211 TGAGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCGCGTTTGTGGGTTTTCGTACAGCAAG 1270  
QY 1261 CACTGGGGATCTTGGTAGATCTGAGTCTGTGTGTGTCGGGTCTGGAATCCCTGCCAAGA 1320  
Db 1271 CACTGGGGATCTTGGTAGATCTGAGTCTGTGTGTGTCGGGTCTGGAATCCCTGCCAAGA 1330  
QY 1321 CTAGCTCCATGGAAGAAACTTCTCATCAAGCAAGAGCTTACAGACTCTCAGGACA 1380  
Db 1331 CTAGCTCCATGGAAGAAACTTCTCATCAAGCAAGAGCTTACAGACTCTCAGGACA 1390  
QY 1381 AGTGTCAAGGT 1393  
Db 1391 AGTGTCAAGAT 1403

RESULT 11  
AAL55214  
ID AAL55214 standard; DNA; 6165 BP.  
XX  
AC AAL55214;  
XX  
DT 01-MAY-2003 (first entry)  
XX Human CR1K encoding DNA sequence, SEQ ID No 1.  
XX  
DE Anorectic; hypotensive; cardiast; antilipaeamic; cerebroprotective;  
XX Antigonut; osteopathic; antiarthritic; cytostatic; antidepressant;  
XX Immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;  
XX Neuroprotective; antinflammatory; antidiabetic; analgesic;  
XX human citron rho/rac-interacting kinase; enzyme; CR1K; ameliorating;  
XX obesity; comorbidities; cancer; anorexia; cachexia; bulimia;  
XX central nervous system disorder; chronic obstructive pulmonary disease;  
XX diabetes; pain; gene; ds.  
XX Homo sapiens.  
XX  
Key Location/Qualifiers  
CDS 1..6165  
FT /tag= a  
FT /product= "Human CR1K protein"  
XX  
PN W02003004523-A1.  
XX  
PD 16-JAN-2003.  
XX  
PF 28-JUN-2002; 2002WO-EP007156.  
XX  
PR 02-JUL-2001; 2001US-0301841P.  
PR 11-DEC-2001; 2001US-0338651P.  
PR 25-APR-2002; 2002US-0375014P.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Zhu Z;  
XX  
DR WPI; 2003-221576/21.  
DR P-PSDB; AAO26959.  
XX  
PT New human citron rho/rac-interacting kinase (CR1K) polypeptide and  
PT polynucleotide, useful in preventing, ameliorating or treating diseases  
PT associated with human CR1K dysfunction, e.g. obesity, diabetes or  
PT Alzheimer's disease.  
XX  
PS Example 1; Fig 1; 237pp; English.  
XX  
CC The invention relates to an isolated polynucleotide encoding a human

citron rho/rac-interacting kinase polypeptide. The isolated polynucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human c165 rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide are useful in preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, prostate and colon cancer), anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease or Alzheimer's disease), chronic obstructive pulmonary disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polynucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This polynucleotide sequence represents a DNA sequence encoding a human CRIK protein of the invention

Sequence 6165 BP: 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other:

Q Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;

Query Match 93.7%: Score 1388.2: DB 9: Length 6165:

Query Match 93.7%: Score 1388.2: DB 9: Length 6165:

Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0

1	Qy	TCAAAATATGGAGCGCGGAATCCTTTGGATGCTGTGCTGAAACCCATTCGCCAACCGGG	60
11	Db	TCAAAATATGGAGCGCGGAATCCTTTGGATGCTGTGCTGCTGAACCCATTCGCCACCGGG	70
61	Qy	CCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCCCTTTATGACTCAAACAGAGATGT	120
71	Db	CCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCCCTTTATGACTCAAACAGCAGATGT	130
121	Qy	CTCCTCTTTCCGAGAAAGGGAATATAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC	180
131	Db	CTCCTCTTTCCGAGAAAGGGAATATAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC	190
181	Qy	AGCCTGCTCTGATCAAGATTAAGACACGTCGACCACTTTGTCGGGAAGTATTTCCGACACCA	240
191	Db	AGCCTGCTCTGATCAAGATTAAGACACGTCGACCACTTTGTCGGGAAGTATTTCCGACACCA	250
241	Qy	TAGCTGAGTTACAGGAGCTCCAGGCTTTGGCAAAGGACTTCGAAGTCAGAAAGTCTTTAG	300
251	Db	TAGCTGAGTTACAGGAGCTCCAGGCTTCGGCAAAGGACTTCGAAGTCAGAAAGTCTTTAG	310
301	Qy	GTTGTGCTCACTTTGCTGAAGTCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG	360
311	Db	GTTGTGCTCACTTTGCTGAAGTCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG	370
361	Qy	CTATGAAGTGTACGAAGAAGGCTTTATTGGCCCGAGCAGCTTTTCATTTTTTGAGG	420
371	Db	CTATGAAGTGTACGAAGAAGGCTTTATTGGCCCGAGCAGCTTTTCATTTTTTGAGG	430
421	Qy	AAGAGCGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTCACGATGCGCT	480
431	Db	AAGAGCGGAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTCACGATGCGCT	490
481	Qy	TTCAGGACAAAAATCACCTTTATCTGGTCATGGAAATATCAGCCTGGAGGGGACTTGCTGT	540
491	Db	TTCAGGACAAAAATCACCTTTATCTGGTCATGGAAATATCAGCCTGGAGGGGACTTGCTGT	550
541	Qy	CACCTTTTGAATAGATATGAGGACCACTTAGATGAAACCTCATACAGTTTTTACCTAGCTG	600
551	Db	CACCTTTTGAATAGATATGAGGACCACTTAGATGAAACCTCATACAGTTTTTACCTAGCTG	610
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611	Db	AGCTGATTTTGGCTGTTTCAACAGCGTTTCACTGTATGGGATACGTGCATCGAGACATCAAGC	670









Qy	841	GTGACTGGTGGTCAGTGGCGGTGATGCCCTATGAGATGATTATGGAGAGATCCCCCTTCG	900
Db	851	GTGACTGGTGGTCAGTGGCGGTGATGCCCTATGAGATGATTATGGAGAGATCCCCCTTCG	910
Qy	901	CAGAGGGAACTCTGCGCAGAACCTTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT	960
Db	911	CAGAGGGAACTCTGCGCAGAACCTTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT	970
Qy	961	TTCAGATGACCCCAAAAGTGAGCAGTGACATTTCTTTGATCTGTATCAAAGCTTCTGTGGC	1020
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Qy	1141	ACACTCCAAATTTTGATGAACACAGAGAAGAATTCGTGGGTTTCATCTCTCCGTGCCAGC	1200
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Qy	1261	CACGTGGGGATTCCTGGTAGATCTGAGTCTGTTGTGTCGGGCTCTGGACTCCCTGCCAAGA	1320
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AC	ADN62808;		
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DT	01-JUL-2004 (first entry)		
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XX	Human NOV1b DNA.		
XX			
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KW	infectious disease; anorexia; cancer; cancer-associated cachexia;		
KW	neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;		
KW	immune disorder; haematopoietic disorder; dyslipidaemia;		
XX	metabolic syndrome X; wasting disorder.		
OS	Homo sapiens.		
XX			
PN	US2004038223-A1.		
XX			
PD	26-FEB-2004.		
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PF	01-OCT-2002; 2002US-00262511.		
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PR	02-OCT-2001; 2001US-0326483P.		
PR	05-OCT-2001; 2001US-0327435P.		
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PR	09-OCT-2001; 2001US-0327917P.		
PR	09-OCT-2001; 2001US-0328029P.		
PR	09-OCT-2001; 2001US-0328044P.		
PR	09-OCT-2001; 2001US-0328056P.		
PR	12-OCT-2001; 2001US-0328849P.		









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Db 737 CGAAATGAATTCAAACAGATGTGAATCCAACTCCCGATTGGGACCCAGATATACA 796  
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RESULT 2  
AR453415  
LOCUS AR453415 1515 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 1 from patent US 680188.  
ACCESSION AR453415  
VERSION AR453415.1 GI:42686143  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1515)  
AUTHORS Webster,M., Yan,C., Di Francesco,V. and Beasley,E.M.  
TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof  
JOURNAL Patent: US 680188-A 1 20-JAN-2004;  
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Best Local Similarity 100.0%; Pred. No. 0;  
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Db 17 TCAATATGGAGCGCGGAATCCTTTGGATGCTGCTGCTGAACCCATTTGCCAACCGGG 76  
Qy 61 CTCTCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGATCTCAACAGCAGATGT 120  
Db 77 CTCTCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGATCTCAACAGCAGATGT 136  
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Db 137 CTCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTTTGAAGATGAGTC 196  
Qy 181 AGCTCTCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCCGAAAGTATTCGACACCA 240  
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Qy 241 TAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAGGACTTCGAAGTCAAGAGTCTTGTAG 300  
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Db 377 CTATGAAGTGATGAAGAGAGGCTTTATTTGGCCCGAGGAGGTTTCATTTTTCAGG 436  
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Db 437 AAGAGCGGAACATATTATCTGAGCACAAGCCCGTGGATCCCGCAATACAGTATGCCT 496  
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RESULT 3  
AX671044  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM







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DB 1451 CCGTATATGCCAAGGATCCCGCGGCGCTGC 1485

RESULT 6  
AR534559  
LOCUS AR534559 5877 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 3 from patent US 6734009.  
ACCESSION AR534559  
VERSION AR534559.1 GI:53924886  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5877)  
AUTHORS Yu,X.S., Miranda,M. and Friddle,C.J.  
TITLE Human kinases and polynucleotides encoding the same  
JOURNAL Patent: US 6734009-A 3 11-MAY-2004;  
FEATURES  
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Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 361 CTATGAAGTGTGAAGAGAGCTTTATTTGCCCCAGGAGAGGTTTCAATTTTGGAG 420  
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QY 421 AAGAGCGGAACATATTTATCTCGAGACAAAGCCGCTGATCCCGCAATTTACAGTATGCT 480  
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QY 1381 AGTGTCACAAGGT 1393  
DB 1391 AGTGTCACAAGAT 1403

RESULT 7  
AX574427  
LOCUS AX574427 5877 bp DNA linear PAT 07-JAN-2003  
DEFINITION Sequence 3 from Patent WO02059325.  
ACCESSION AX574427  
VERSION AX574427.1 GI:27551752  
KEYWORDS Homo sapiens (human)  
SOURCE

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VERSION	AX671112.1		
KEYWORDS	GI:29329572		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Zhu, Z.		
TITLE	Regulation of human citron rho/rac-interacting kinase		
JOURNAL	Patent: WO 03004523-A 8 16-JAN-2003;		
FEATURES	Bayer Aktiengesellschaft (DE)		
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RESULT 12
AX504254
LOCUS AX504254 6298 bp DNA linear PAT 27-SBP-2002
DEFINITION Sequence 43 from Patent WO0233099.
ACCESSION AX504254
VERSION AX504254.1 GI:23386094
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gururajan,R., Baughn,M.R., Wallia,N.K., Elliott,V.S., Xu,Y.,
Arvisu,C., Yao,M.G., Ramkumar,J., Ding,L., Tang,Y.T., Hafalia,A.J.,
Nguyen,D.B., Gandhi,A.R., Lu,Y., Yue,H., Burford,N., Bandman,O.,
Tribouley,C.M., Lal,P.G., Recipon,S.A., Lu,D.A., Borowsky,M.L.,
Thornton,M., Swarnaker,A., Thangavelu,K., Khan,F.A. and Ison,C.H.
Human kinases
TITLE Patent: WO 0233099-A 43 25-APR-2002;
JOURNAL Incyte Genomics, Inc. (US)
FEATURES
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Best Local Similarity 99.8%; Pred. No. 0;
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ACCESSION AY209000
VERSION AY209000.1 GI:37784566
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1799)
AUTHORS Mao, Y., Xie, Y. and Wu, Q.
TITLE Cloning and characterizing a novel human CR1K-SK gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1799)
AUTHORS Mao, Y., Xie, Y. and Wu, Q.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2003) Institute of Genetics, Fudan University,
220 Handan Road, Shanghai 200433, P.R. China

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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#### SUMMARIES

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#### ALIGNMENTS

#### RESULT 1

US-09-804-471A-1  
; Sequence 1, Application US/09804471A

; Patent No. US20020132322A1

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: CLO01164

; CURRENT APPLICATION NUMBER: US/09/804, 471A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1515

; TYPE: DNA

; ORGANISM: Human

; US-09-804-471A-1

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Db 1021 CAAAGCTTTGTTGGCGGCAGAAAGAGAGACTGAAAGTTGAAAGTCTTTGTCGCATCT 1080  
Qy 1081 TTTCTTCTTAAATTTGACTGGAACAACTTCTGTAATCTCTCCCTCCCTTCTGTTCCAC 1140  
Db 1081 TTTCTTCTTAAATTTGACTGGAACAACTTCTGTAATCTCTCCCTCCCTTCTGTTCCAC 1140  
Qy 1141 CTCAGTCCGAGATGACACTTCAATTTTGTATGAACAGAGAAATTCGTGGGTTTCA 1200  
Db 1141 CTCAGTCCGAGATGACACTTCAATTTTGTATGAACAGAGAAATTCGTGGGTTTCA 1200  
Qy 1201 TCTCTCCGTCGAGCTGAGCCCTCAGCCTTCTCGGTTGAAGAACTGCGGTTTGTGGG 1260  
Db 1201 TCTCTCCGTCGAGCTGAGCCCTCAGCCTTCTCGGTTGAAGAACTGCGGTTTGTGGG 1260

Qy 1261 TTTTCGTACAGCAAGGCACTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTGCGGTCG 1320  
Db 1261 TTTTCGTACAGCAAGGCACTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTGCGGTCG 1320  
Qy 1321 GACTCCCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTA 1380  
Db 1321 GACTCCCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTA 1380  
Qy 1381 CAAGACTCTCAGACACAGTGTCAAGGTATTTATTTCCGACCGCGCTTCCTTCTTGC 1440  
Db 1381 CAAGACTCTCAGACACAGTGTCAAGGTATTTATTTCCGACCGCGCTTCCTTCTTGC 1440  
Qy 1441 TCCAGGATCTCCCGTCCGTATATGCAAGGATCCGCGCGGCGCTGCTGGCTCTGA 1500  
Db 1441 TCCAGGATCTCCCGTCCGTATATGCAAGGATCCGCGCGGCGCTGCTGGCTCTGA 1500  
Qy 1501 GCCGCTGATCCGTA 1515  
Db 1501 GCCGCTGATCCGTA 1515

RESULT 2

US-10-238-709-1  
; Sequence 1, Application US/10238709  
; Publication No. US20030022340A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; CURRENT FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Human  
US-10-238-709-1

Query Match 100.0%; Score 1515; DB 14; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGAGATGTTGAAGTTCAAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGTCTGAA 60  
Db 1 GGGGAGATGTTGAAGTTCAAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGTCTGAA 60  
Qy 61 CCCATTGCCAACCCGGGCTCCAGGCTGAATCTGTTTCCAGGGGAAACCAACCTTTATG 120  
Db 61 CCCATTGCCAACCCGGGCTCCAGGCTGAATCTGTTTCCAGGGGAAACCAACCTTTATG 120  
Qy 121 ACTCAACAGCAGATGTCTCTCTTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTC 180  
Db 121 ACTCAACAGCAGATGTCTCTCTTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTC 180  
Qy 181 TTTGAAGATGCACTGACCTGCTCTGATGAAGATTAAGACAGTGAACATTTGTTCGG 240  
Db 181 TTTGAAGATGCACTGACCTGCTCTGATGAAGATTAAGACAGTGAACATTTGTTCGG 240  
Qy 241 AAGTATTTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAA 300  
Db 241 AAGTATTTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAA 300  
Qy 301 GTCAGAGTCTTGTAGGTTGTGGTCACTTTCTGTAAGTGCAGGTGGTAAAGAGAAAGCA 360  
Db 301 GTCAGAGTCTTGTAGGTTGTGGTCACTTTCTGTAAGTGCAGGTGGTAAAGAGAAAGCA 360  
Qy 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGGCCACAGGACAG 420  
Db 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGGCCACAGGACAG 420

Qy 421 GTTTCATTTTGTAGGAAGCGGAAACATATTAATCTCGAAGCAACAGCCCGTGGATCCCC 480  
Db |||||||  
Qy 421 GTTTCATTTTGTAGGAAGCGGAAACATATTAATCTCGAAGCAACAGCCCGTGGATCCCC 480  
Db |||||||  
Qy 481 CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCCT 540  
Db |||||||  
Qy 481 CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCCT 540  
Db |||||||  
Qy 541 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATCAGGACAGATTAGATGAATAAAGCTGATA 600  
Db |||||||  
Qy 541 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATCAGGACAGATTAGATGAATAAAGCTGATA 600  
Db |||||||  
Qy 601 CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTCAACAGCGTTTCTATCTGATGGGATAGTG 660  
Db |||||||  
Qy 601 CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTCAACAGCGTTTCTATCTGATGGGATAGTG 660  
Db |||||||  
Qy 661 CATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGCACAGGACATCAAGCTGGTG 720  
Db |||||||  
Qy 661 CATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGCACAGGACATCAAGCTGGTG 720  
Db |||||||  
Qy 721 GATTTTGGATCTGCGCGGAAATGAATTCAAAAGAGTGGTGAATGCAAACTCCCGATT 780  
Db |||||||  
Qy 721 GATTTTGGATCTGCGCGGAAATGAATTCAAAAGAGTGGTGAATGCAAACTCCCGATT 780  
Db |||||||  
Qy 781 GGGACCCAGATTACATGGCTCTGAAAGTGTCTGATGTAACGGGGATGGAAGGC 840  
Db |||||||  
Qy 781 GGGACCCAGATTACATGGCTCTGAAAGTGTCTGATGTAACGGGGATGGAAGGC 840  
Db |||||||  
Qy 841 ACCTAGCCCTGAGCTGTGATGCTGTGAGTGTGAGTGGCGGTGATTTGCTATGATGATTTAT 900  
Db |||||||  
Qy 841 ACCTAGCCCTGAGCTGTGATGCTGTGAGTGTGAGTGGCGGTGATTTGCTATGATGATTTAT 900  
Db |||||||  
Qy 901 GGGAGATCCCTTCGCGAGAGGAACTCTGCCAGAACCTTCAATAACATTTATGAATTC 960  
Db |||||||  
Qy 901 GGGAGATCCCTTCGCGAGAGGAACTCTGCCAGAACCTTCAATAACATTTATGAATTC 960  
Db |||||||  
Qy 961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGTGAGTGTGATTTCTTTGATCTGATT 1020  
Db |||||||  
Qy 1021 CAAAGCTTGTGTGCGGCGAAGAGAGAGACTGAAGTTTGAAGTCTTTTGTGCTGCAATCT 1080  
Db |||||||  
Qy 1021 CAAAGCTTGTGTGCGGCGAAGAGAGAGACTGAAGTTTGAAGTCTTTTGTGCTGCAATCT 1080  
Db |||||||  
Qy 1081 TTCTTCTTAAATTTGACTGGAACAACTTCGTAACCTCTCTCCCGCTTCTGTTTCCACCC 1140  
Db |||||||  
Qy 1081 TTCTTCTTAAATTTGACTGGAACAACTTCGTAACCTCTCTCCCGCTTCTGTTTCCACCC 1140  
Db |||||||  
Qy 1141 CTCAAGTCCGACGATGACACTCCAAATTTTGTAGTGAACAGAGAAATTCGTGGGTTTCA 1200  
Db |||||||  
Qy 1141 CTCAAGTCCGACGATGACACTCCAAATTTTGTAGTGAACAGAGAAATTCGTGGGTTTCA 1200  
Db |||||||  
Qy 1201 TCCTTCCGTCGACGTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGG 1260  
Db |||||||  
Qy 1201 TCCTTCCGTCGACGTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGG 1260  
Db |||||||  
Qy 1261 TTTTTCGTACAGGACGACCTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTTGCGGCTCTG 1320  
Db |||||||  
Qy 1261 TTTTTCGTACAGGACGACCTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTTGCGGCTCTG 1320  
Db |||||||  
Qy 1321 GACTCCCTGCCAAGACTAGCTCCATGTAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
Db |||||||  
Qy 1321 GACTCCCTGCCAAGACTAGCTCCATGTAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
Db |||||||  
Qy 1381 CAAGACTCTCAGGACAAAGTGTCAAGAGTATTTATTTCCGAGCCGCGCTCTTCTTCTTGC 1440  
Db |||||||  
Qy 1381 CAAGACTCTCAGGACAAAGTGTCAAGAGTATTTATTTCCGAGCCGCGCTCTTCTTCTTGC 1440  
Db |||||||  
Qy 1441 TCCAGGATCTCCGCTCCGTTATATGCCAAGGATTCGCGCCGCGGCGCTGCTGCTCTGA 1500  
Db |||||||  
Qy 1441 TCCAGGATCTCCGCTCCGTTATATGCCAAGGATTCGCGCCGCGGCGCTGCTGCTCTGA 1500  
Db |||||||

RESULT 3  
US-10-724-594-1  
; Sequence 1, Application US/10724594  
; Publication No. US20040091993A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USBS  
; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001164DIV II  
; CURRENT APPLICATION NUMBER: US/10/724,594  
; CURRENT FILING DATE: 2003-12-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-724-594-1

Query Match 100.0%; Score 1515; DB 17; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCTCTTTGGATGCTGTGCTGAA 60  
Db |||||||  
Qy 1 GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCTCTTTGGATGCTGTGCTGAA 60  
Db |||||||  
Qy 61 CCATTTGCCAACCGGCGCTCCAGCTGAACTCTTCTCCAGGGGAACCACTTTATG 120  
Db |||||||  
Qy 61 CCATTTGCCAACCGGCGCTCCAGCTGAACTCTTCTCCAGGGGAACCACTTTATG 120  
Db |||||||  
Qy 121 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGAGGATATAGATGCCCTCTTTGTTCTC 180  
Db |||||||  
Qy 121 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGAGGATATAGATGCCCTCTTTGTTCTC 180  
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Qy 181 TTTGAAGAATGCACTGAGTGTGCTGATGAAGATTAAGCACTGAGCAACTTTGTCGG 240  
Db |||||||  
Qy 181 TTTGAAGAATGCACTGAGTGTGCTGATGAAGATTAAGCACTGAGCAACTTTGTCGG 240  
Db |||||||  
Qy 241 AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCGCAAGAGGACTTCGAA 300  
Db |||||||  
Qy 241 AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCGCAAGAGGACTTCGAA 300  
Db |||||||  
Qy 301 GTCAGAAAGTCTGTAGTGTGCTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAAAGCA 360  
Db |||||||  
Qy 301 GTCAGAAAGTCTGTAGTGTGCTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAAAGCA 360  
Db |||||||  
Qy 361 ACCGGGAGCATCTATGCTATGAAGTGAAGAAGAGGCTTTATTTGGCCAGGAGCAG 420  
Db |||||||  
Qy 361 ACCGGGAGCATCTATGCTATGAAGTGAAGAAGAGGCTTTATTTGGCCAGGAGCAG 420  
Db |||||||  
Qy 421 GTTTTCATTTTTCAGGAGAGCGGAAACATATTAATCTCGAAGCAACAGCCCGTGGATCCCC 480  
Db |||||||  
Qy 421 GTTTTCATTTTTCAGGAGAGCGGAAACATATTAATCTCGAAGCAACAGCCCGTGGATCCCC 480  
Db |||||||  
Qy 481 CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCCT 540  
Db |||||||  
Qy 481 CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCCT 540  
Db |||||||  
Qy 541 GGAGGGAGCTTGTGCTGCTCACTTTTGAATAGATATGAGGACAGTTAGATGAAGAACTGATA 600  
Db |||||||  
Qy 541 GGAGGGAGCTTGTGCTGCTCACTTTTGAATAGATATGAGGACAGTTAGATGAAGAACTGATA 600  
Db |||||||  
Qy 601 CAGTTTTCCTAGCTAGCTGATTTTGGCTGTTTCAAGGCTTCTATCTGATGGGATAGCTG 660  
Db |||||||  
Qy 601 CAGTTTTCCTAGCTAGCTGATTTTGGCTGTTTCAAGGCTTCTATCTGATGGGATAGCTG 660  
Db |||||||







US-10-415-011-43

Query Match	92.78;	Score 1404.2;	DB 17;	Length 6298;
Best Local Similarity	99.84;	Pred. No. 0;		
Matches 1406;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	GGGAGAGTGTGAAGTTCAATATGAGCGCGGAATCCTTTGGATGCTGGTGTGCTGAA	60	
DB	49	GGGAGAGTGTGAAGTTCAATATGAGCGCGGAATCCTTTGGATGCTGGTGTGCTGAA	108	
QY	61	CCATTGCCAACCGGGCTCCAGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATG	120	
DB	109	CCATTGCCAGCGGGCTCCAGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATG	168	
QY	121	ACTCAACAGCAGATGCTCTCTCTTCCGAGAGGGATATTAGATGCCCTTTGTCTC	180	
DB	169	ACTCAACAGCAGATGCTCTCTCTTCCGAGAGGGATATTAGATGCCCTTTGTCTC	228	
QY	181	TTTGAAGAAATGCAGTCAAGCTGCTCTGATGAAGATTAAAGCACGTGAGCAACTTTGTCGG	240	
DB	229	TTTGAAGAAATGCAGTCAAGCTGCTCTGATGAAGATTAAAGCACGTGAGCAACTTTGTCGG	288	
QY	241	AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAAAGGACTTCGAA	300	
DB	289	AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAAAGGACTTCGAA	348	
QY	301	GTCAAGATCTTGTAGTGTGCTCACTTTCTGAGTGCAGTGGTGAAGAGAAAGCA	360	
DB	349	GTCAAGATCTTGTAGTGTGCTCACTTTCTGAGTGCAGTGGTGAAGAGAAAGCA	408	
QY	361	ACCGGGACATCTATGCTATGAAGTGAAGAAAGGCTTTATTGGCCCGAGGAGCAG	420	
DB	409	ACCGGGACATCTATGCTATGAAGTGAAGAAAGGCTTTATTGGCCCGAGGAGCAG	468	
QY	421	GTTCATTTTTTGGAGAGAGCGGAAATATTATCTCGAAGCAACAGCCCGTGATCCCC	480	
DB	469	GTTCATTTTTTGGAGAGAGCGGAAATATTATCTCGAAGCAACAGCCCGTGATCCCC	528	
QY	481	CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGTCATGGAATATCAGCCT	540	
DB	529	CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGTCATGGAATATCAGCCT	588	
QY	541	GGAGGGACATCTGCTCACTTTTGAATAGATATGAGCACAGTGTAGATGAACCTGATA	600	
DB	589	GGAGGGACATCTGCTCACTTTTGAATAGATATGAGCACAGTGTAGATGAACCTGATA	648	
QY	601	CAGTTTACCTAGCTAGCTGATTTTGGCTGTTCAACAGCTTCATCTGTATGGGATACGTG	660	
DB	649	CAGTTTACCTAGCTAGCTGATTTTGGCTGTTCAACAGCTTCATCTGTATGGGATACGTG	708	
QY	661	CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGACACATCAAGCTGGTG	720	
DB	709	CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGACACATCAAGCTGGTG	768	
QY	721	GATTTTGGATCTGCGCGGAAATGAATTCAAAAGATGGTGAATGCCAACTCCCGATT	780	
DB	769	GATTTTGGATCTGCGCGGAAATGAATTCAAAAGATGGTGAATGCCAACTCCCGATT	828	
QY	781	GGGACCCAGATTAATGAGTTCCTGAAAGTGTGATGTAACGGGGATGGAAGAGGC	840	
DB	829	GGGACCCAGATTAATGAGTTCCTGAAAGTGTGATGTAACGGGGATGGAAGAGGC	888	
QY	841	ACCTACGGCTGGAATGATGCTGGTGTGCTGAGTGGCGGTGATGCTATGAGATGATTAT	900	
DB	889	ACCTACGGCTGGAATGATGCTGGTGTGCTGAGTGGCGGTGATGCTATGAGATGATTAT	948	
QY	901	GGGAGATCCCTTCGACAGAGGGAACCTCTGCGCAGAAACCTTCAATACATTATGAATTC	960	
DB	949	GGGAGATCCCTTCGACAGAGGGAACCTCTGCGCAGAAACCTTCAATACATTATGAATTC	1008	
QY	961	CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAATCTTTCTGTGATCTGATT	1020	
DB	1009	CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAATCTTTCTGTGATCTGATT	1068	

Qy	1021	CRAAGCTTGTGTGCGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT	1080
Db	1069	CRAAGCTTGTGTGCGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT	1128
Qy	1081	TTCTTCTTAAATTTGACTGGAAACAACATTGTAATCTCTCCCTCCCTTCGTTCCACC	1140
Db	1129	TTCTTCTTAAATTTGACTGGAAACAACATTGTAATCTCTCCCTCCCTTCGTTCCACC	1188
Qy	1141	CTCAAGTCCGACATGACACCTCCAAATTTTGAAGAACAGAGAAATTCGTGGGTTTCA	1200
Db	1189	CTCAAGTCCGACATGACACCTCCAAATTTTGAAGAACAGAGAAATTCGTGGGTTTCA	1248
Qy	1201	TCCTCTCCGTGCGAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGG	1260
Db	1249	TCCTCTCCGTGCGAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGG	1308
Qy	1261	TTTTCTGACAGCAAGCACTGGGGATTTCTTGGTAGATCTGAGTCTGTGTGCGGTCTG	1320
Db	1309	TTTTCTGACAGCAAGCACTGGGGATTTCTTGGTAGATCTGAGTCTGTGTGCGGTCTG	1368
Qy	1321	GACTCCCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTA	1380
Db	1369	GACTCCCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTA	1428
Qy	1381	CRAAGCTCTCAGGACAAAGTGTCAAAAGT	1409
Db	1429	CRAAGCTCTCAGGACAAAGTGTCAAAAGT	1457

RESULT 6

US-10-262-511-3  
; Sequence 3, Application US/10262511  
; Publication No. US20040038223A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John A.  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Ju, Jingfang  
; APPLICANT: Li, Li  
; APPLICANT: Guo, Xiaojia (Sasha)  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Ort, Tatiana  
; APPLICANT: Gorman, Linda  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Catterton, Elina  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Stone, David J.  
; APPLICANT: Pena, Carol E. A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Rothenberg, Mark E.  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Agee, Michele L.  
; APPLICANT: Berghs, Constance  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-462C  
; CURRENT APPLICATION NUMBER: US/10/262,511  
; PRIOR FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: 60/326,483  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: 60/373,815  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/327,917

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; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 3
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1870)
US-10-262-511-3

Query Match          92.3%; Score 1398.2; DB 17; Length 1870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGTTGAAGTTCAAATATGAGCGCGCGAATCCCTTTGGATGCTGGTCTGCTGAACCCATT 66
DB 14 ATGTTGAAGTTCAAATATGAGCGCGCGAATCCCTTTGGATGCTGGTCTGCTGAACCCATT 73
QY 67 GCCAACCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAA 126
DB 74 GCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAA 133
QY 127 CAGCAGATCTCTCTCTTCCGAGAGGATATAGATGCTCTCTCTCTCTCTCTCTTGA 186
DB 134 CAGCAGATCTCTCTCTTCCGAGAGGATATAGATGCTCTCTCTCTCTCTCTTGA 193
QY 187 GAATGAGTCTGCTCTCTCTGATGAAGATTAAGCAGCTGAGCAACTTTTTCGCGAAGTAT 246
DB 194 GAATGAGTCTGCTCTCTCTGATGAAGATTAAGCAGCTGAGCAACTTTTTCGCGAAGTAT 253
QY 247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCCGCGAAAGCACTTCGAAAGTCAGA 306
DB 254 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCCGCGAAAGCACTTCGAAAGTCAGA 313
QY 307 AGTCTTGTAGTGTGCTGCTCTCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 366
DB 314 AGTCTTGTAGTGTGCTGCTCTCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 373
QY 367 GACATCTATGCTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCCGAGGAGAGGTTTCA 426
DB 374 GACATCTATGCTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCCGAGGAGAGGTTTCA 433
QY 427 TTTTGTGAGGAGAGCGGCAATATTTATCTCGAAGCAAGCCGCTGGATGCCCAATTA 486
DB 434 TTTTGTGAGGAGAGCGGCAATATTTATCTCGAAGCAAGCCGCTGGATGCCCAATTA 493
QY 487 CAGTATGCTTTCCAGACAAAATACCTTTATCTGCTATGCTATGCTATGCTATGCTATGCTATGCT 546
DB 494 CAGTATGCTTTCCAGACAAAATACCTTTATCTGCTATGCTATGCTATGCTATGCTATGCTATGCT 553
QY 547 GACTTCTGTCTCTTTTGAATAGATATGAGGACAGTATGAGTGAAGCAACCTGATACAGTTT 606
DB 554 GACTTCTGTCTCTTTTGAATAGATATGAGGACAGTATGAGTGAAGCAACCTGATACAGTTT 613
QY 607 TACTAGCTGAGCTGATTTTGGCTGTTTCCAGGCTTCATCTGATGGGATACGTCATCGA 666
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DB 614 TACCTAGCTGAGCTGATTTTGGCTGTTTCCAGCGCTTCATCTGATGGGATACGTCGATCGA 673
QY 667 GACATCAAGCCTGAGAAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726
DB 674 GACATCAAGCCTGAGAAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 733
QY 727 GGATCTGCGCGGAAATGAATTTCAAACAAGATGGTGAATGCCAAATCTCCGATTTGGGACC 786
DB 734 GGATCTGCGCGGAAATGAATTTCAAACAAGATGGTGAATGCCAAATCTCCGATTTGGGACC 793
QY 787 CCAGATTACATGCTCTGAACTGCTGAGTGAAGCGGATGGAAGGACACCTAC 846
DB 794 CCAGATTACATGCTCTGAACTGCTGAGTGAAGCGGATGGAAGGACACCTAC 853
QY 847 GGCCTGGACTGTGACTGTGGTGTGAGTGGCGGTGATTCCTATGAGATGATTTATGGGAGA 906
DB 854 GGCCTGGACTGTGACTGTGGTGTGAGTGGCGGTGATTCCTATGAGATGATTTATGGGAGA 913
QY 907 TCCCCCTTCGCAGAGGGAACTCTGCGCAAACTTCAATTAACATTAATTAATTTCCAGCGG 966
DB 914 TCCCCCTTCGCAGAGGGAACTCTGCGCAAACTTCAATTAACATTAATTAATTTCCAGCGG 973
QY 967 TTTTGAATTTCCAGATGACCCCAAGTGAGCGAGTGTCTTCTGATCTGATTTCAAGC 1026
DB 974 TTTTGAATTTCCAGATGACCCCAAGTGAGCGAGTGTCTTCTGATCTGATTTCAAGC 1033
QY 1027 TTGTTGTGCGGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTTTCTTTC 1086
DB 1034 TTGTTGTGCGGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTTTCTTTC 1093
QY 1087 TCTAAATTTGACTGGAACCAATTCGTAACTCTCTCTCCCCCTTCGTTCCACCCCTCAAG 1146
DB 1094 TCTAAATTTGACTGGAACCAATTCGTAACTCTCTCTCCCCCTTCGTTCCACCCCTCAAG 1153
QY 1147 TCCGAGATGACACCTCCAAATTTTGAATGACAGAGAAAGTTCGTTGGTTCATCTCT 1206
DB 1154 TCTGACGATGACACCTCCAAATTTTGAATGACAGAGAAAGTTCGTTGGTTCATCTCT 1213
QY 1207 CCGTGCAGCTCAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGGGTTTTCG 1266
DB 1214 CCGTGCAGCTCAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGGGTTTTCG 1273
QY 1267 TACAGCAAGGCACTGGGATTTCTGGTAGATCTGAGTCTGTTGTGCTGGGTCTGGACTCC 1326
DB 1274 TACAGCAAGGCACTGGGATTTCTGGTAGATCTGAGTCTGTTGTGCTGGGTCTGGACTCC 1333
QY 1327 CTGCGCAAGACTAGCTCCATGGAAGAAAGTTCCTCTCATCAAGCAAGAGCTACAGAC 1386
DB 1334 CTGCGCAAGACTAGCTCCATGGAAGAAAGTTCCTCTCATCAAGCAAGAGCTACAGAC 1393
QY 1387 TCTCAGGACAAAGTGTCAAAAGGT 1409
DB 1394 TCTCAGGACAAAGTGTCAAAAGT 1416
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## RESULT 7

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US-10-028-946-3
; Sequence 3, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Fridle, Carl Johan
; APPLICANT: Miranda, Maricar
; TITLE OF INVENTION: No. US20020123622A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
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; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3

Query Match      92.3%; Score 1398.2; DB 13; Length 5877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  7  ATGTTGAAGTTCAAATATGAGCGCGGAATCTCTTTGGATGCTGGTGTGCTGCAACCAATT 66
Db   |
QY  1  ATGTTGAAGTTCAAATATGAGCGCGGAATCTCTTTGGATGCTGGTGTGCTGCAACCAATT 60
Db   |
QY  67  GCCAACCGGGCTCCAGCTGAATCTCTTCCAGGGGAAACCAACCTTTATGACTCAA 126
Db   |
QY  61  GCCAGCGGGCTCCAGCTGAATCTCTTCCAGGGGAAACCAACCTTTATGACTCAA 120
Db   |
QY  127  CAGCAGATGCTCTCTCTTCCAGGAGGATATAGATAGATAGATAGATAGATAGATAGATAGAT 186
Db   |
QY  121  CAGCAGATGCTCTCTCTTCCAGGAGGATATAGATAGATAGATAGATAGATAGATAGATAGAT 180
Db   |
QY  187  GAATGCAGTCAGCTCTCTCTTCCAGGAGGATATAGATAGATAGATAGATAGATAGATAGAT 246
Db   |

Query Match      92.3%; Score 1398.2; DB 18; Length 5877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  7  ATGTTGAAGTTCAAATATGAGCGCGGAATCTCTTTGGATGCTGGTGTGCTGCAACCAATT 66
Db   |
QY  1  ATGTTGAAGTTCAAATATGAGCGCGGAATCTCTTTGGATGCTGGTGTGCTGCAACCAATT 60
Db   |
QY  67  GCCAACCGGGCTCCAGCTGAATCTCTTCCAGGGGAAACCAACCTTTATGACTCAA 126
Db   |
QY  61  GCCAGCGGGCTCCAGCTGAATCTCTTCCAGGGGAAACCAACCTTTATGACTCAA 120
Db   |
QY  127  CAGCAGATGCTCTCTCTTCCAGGAGGATATAGATAGATAGATAGATAGATAGATAGATAGAT 186
Db   |
QY  121  CAGCAGATGCTCTCTCTTCCAGGAGGATATAGATAGATAGATAGATAGATAGATAGATAGAT 180
Db   |
QY  187  GAATGCAGTCAGCTCTCTCTTCCAGGAGGATATAGATAGATAGATAGATAGATAGATAGAT 246
Db   |

; US-10-791-666-3
; Sequence 3, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-791-666-3

RESULT 8
US-10-791-666-3
; Sequence 3, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-791-666-3

961  TTTTGAATTTCCAGATGACCCCAAGTGAGCGATGACTTCTTCTGATCTGATCTCAAGC 1020
1027  TTGTTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTTTGTGCTGCCATCCTTTCTTC 1086
1021  TTGTTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTTTGTGCTGCCATCCTTTCTTC 1080
1087  TCTAAATTTGACTGGAACAACATTCCTAACTCTCTCCCTCCCTTCCCTCCACCTCAAG 1146
1081  TCTAAATTTGACTGGAACAACATTCCTAACTCTCTCCCTCCCTTCCCTCCACCTCAAG 1140
1147  TCCGACATGACACCTCCCAATTTTGTATGAACAGAGAGAAATTCGTGGGTTTCATCTCT 1206
1141  TCTGACATGACACCTCCCAATTTTGTATGAACAGAGAGAAATTCGTGGGTTTCATCTCT 1200
1207  CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTGTGGGTTTTCG 1266
1201  CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTGTGGGTTTTCG 1260
1267  TACAGCAAGGCATCGGGATTTCTGTAGATCTGAGTCTGTGTGTGCTGGTCTGGACTCC 1326
1261  TACAGCAAGGCATCGGGATTTCTGTAGATCTGAGTCTGTGTGTGCTGGTCTGGACTCC 1320
1327  CCGTCCAGAGTAGCTCCATGGAAAAGAACTTCTCATCAAAAGCAAGAGCTACAAGAC 1386
1321  CCGTCCAGAGTAGCTCCATGGAAAAGAACTTCTCATCAAAAGCAAGAGCTACAAGAC 1380
1387  TCTCAGCAAGAGTGTCAAGGT 1409
1381  TCTCAGCAAGAGTGTCAAGAT 1403

; US-10-791-666-3
; Sequence 3, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-791-666-3

Query Match      92.3%; Score 1398.2; DB 18; Length 5877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  7  ATGTTGAAGTTCAAATATGAGCGCGGAATCTCTTTGGATGCTGGTGTGCTGCAACCAATT 66
Db   |
QY  1  ATGTTGAAGTTCAAATATGAGCGCGGAATCTCTTTGGATGCTGGTGTGCTGCAACCAATT 60
Db   |
QY  67  GCCAACCGGGCTCCAGCTGAATCTCTTCCAGGGGAAACCAACCTTTATGACTCAA 126
Db   |
QY  61  GCCAGCGGGCTCCAGCTGAATCTCTTCCAGGGGAAACCAACCTTTATGACTCAA 120
Db   |
QY  127  CAGCAGATGCTCTCTCTTCCAGGAGGATATAGATAGATAGATAGATAGATAGATAGATAGAT 186
Db   |
QY  121  CAGCAGATGCTCTCTCTTCCAGGAGGATATAGATAGATAGATAGATAGATAGATAGATAGAT 180
Db   |
QY  187  GAATGCAGTCAGCTCTCTCTTCCAGGAGGATATAGATAGATAGATAGATAGATAGATAGAT 246
Db   |
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181 GAAATGAGTCAAGCTGCTCTGATCAAGATTAAGCAAGCTGAGCAACTTTGTCCGGAAGTAT 240  
247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGSCAAAGGACCTTCGAAGTCAGA 306  
241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGSCAAAGGACCTTCGAAGTCAGA 300  
307 AGTCTTTAGGTTGTGCTCACTTTGTCTGAAAGTGCAGGTGTAAGAGAGAAAGCAACCGGG 366  
301 AGTCTTTAGGTTGTGCTCACTTTGTCTGAAAGTGCAGGTGTAAGAGAGAAAGCAACCGGG 360  
367 GACATCTATGCTATGAAGTGTAGAGAGAAAGGCTTTATTGGCCCGAGGAGAGGTTTCA 426  
361 GACATCTATGCTATGAAGTGTAGAGAGAAAGGCTTTATTGGCCCGAGGAGAGGTTTCA 420  
427 TTTTGTGAGGAGAGCGGACATATTATCTCGAAGCACAAGCCCTGCGATCCCCCAATTA 486  
421 TTTTGTGAGGAGAGCGGACATATTATCTCGAAGCACAAGCCCTGCGATCCCCCAATTA 480  
487 CAGTATGCTTTCCAGGACAAAATACCTTTATCTGTCATGGAATATCAGCCTGGAGGG 546  
481 CAGTATGCTTTCCAGGACAAAATACCTTTATCTGTCATGGAATATCAGCCTGGAGGG 540  
547 GACTTGTCTCACTTTTGAATAGATAGAGGACAGTTAGATGAAGAACTTGATACAGTTT 606  
541 GACTTGTCTCACTTTTGAATAGATAGAGGACAGTTAGATGAAGAACTTGATACAGTTT 600  
607 TACCTAGCTGAGCTGATTTGGCTGTTTCCAGCGTTCATCTGATGGATACGTCGATCGA 666  
601 TACCTAGCTGAGCTGATTTGGCTGTTTCCAGCGTTCATCTGATGGATACGTCGATCGA 660  
667 GACATCAAGCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGAATTT 726  
661 GACATCAAGCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGAATTT 720  
727 GGATCTGCCCGGAAATGAATTAACAAGATGGTGAATGCCAACTCCGATTTGGGACC 786  
721 GGATCTGCCCGGAAATGAATTAACAAGATGGTGAATGCCAACTCCGATTTGGGACC 780  
787 CCAGATTAACATGCTCTGAGTGGCTGAGTGGGCTGATTTGCCCTATGAGATGATTTATGGAGA 846  
781 CCAGATTAACATGCTCTGAGTGGCTGAGTGGGCTGATTTGCCCTATGAGATGATTTATGGAGA 840  
847 GGCTTGAGCTGCTGACTGGTGGTCACTGGGCGTGAATGGCTATGAGATGATTTATGGAGA 906  
841 GGCTTGAGCTGCTGACTGGTGGTCACTGGGCGTGAATGGCTATGAGATGATTTATGGAGA 900  
907 TCCCTCTTCGACAGGGAACCTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 966  
901 TCCCTCTTCGACAGGGAACCTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 960  
967 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATTTCAAGC 1026  
961 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATTTCAAGC 1020  
1027 TTGTTGTGGCCGACAGAGAGACTGAAGTTTGAAGTCTTGTCTGCCATCTCTTCTTC 1086  
1021 TTGTTGTGGCCGACAGAGAGACTGAAGTTTGAAGTCTTGTCTGCCATCTCTTCTTC 1080  
1087 TCTAAATTAAGTGAAGAACCAATTCGTAATCTCTCCCTCCCTTCGTTCCACCTCAAG 1146  
1081 TCTAAATTAAGTGAAGAACCAATTCGTAATCTCTCCCTCCCTTCGTTCCACCTCAAG 1140  
1147 TCCGACGATGACACCTTCAATTTTGAATGAACGAGAGAAATTCGTGGGTTTCACTCTCT 1206  
1141 TCTGACGATGACACCTTCAATTTTGAATGAACGAGAGAAATTCGTGGGTTTCACTCTCT 1200  
1207 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGGGTTTTCG 1266  
1201 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGGGTTTTCG 1260  
1267 TACAGCAAGGCACTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTGTCGGGCTGAGACTCC 1326

1261 TACAGCAAGGCACTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTGTCGGGCTTGGACTCC 1320  
1327 CTTGCCAAGACTAGCTCCATGGAAGAAACTTTCTCATCAAAAGCAAGAGCTACAAGAC 1386  
1321 CTTGCCAAGACTAGCTCCATGGAAGAAACTTTCTCATCAAAAGCAAGAGCTACAAGAC 1380  
1387 TCTCAGCAAGTGTCTCAAGGT 1409  
1381 TCTCAGCAAGTGTCAAGAT 1403

RESULT 9  
US-10-028-946-1  
; Sequence 1, Application US/10028946  
; Publication No. US20020123622A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 6165  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-028-946-1

Query Match 92.3%; Score 1398.2; DB 13; Length 6165;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

7 ATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAAACCCATT 66  
1 ATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAAACCCATT 60  
67 GCCAACCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAA 126  
61 GCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAA 120  
127 CAGCAGATGCTCTCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTTTTGA 186  
121 CAGCAGATGCTCTCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTTTTGA 180  
187 GAATGCAGTCAGCTCTCTCTGATGAAGATTAAGCAGCTGAGCAACTTTTGTCCGGAAGTAT 246  
181 GAATGCAGTCAGCTCTCTCTGATGAAGATTAAGCAGCTGAGCAACTTTTGTCCGGAAGTAT 240  
247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCGCAAGAGACTTCGAAGTCAGA 306  
241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCGCAAGAGACTTCGAAGTCAGA 300  
307 AGTCTTGTAGTGTGGTCACTTTGCTGAAGTCAGTGGTGAAGAGAGAAAGCAACCGGG 366  
301 AGTCTTGTAGTGTGGTCACTTTGCTGAAGTCAGTGGTGAAGAGAGAAAGCAACCGGG 360  
367 GACATCTATGCTATGAAGTGTGAAGAGAGAGGCTTTATTGGCCCGAGGAGAGGTTTCA 426  
361 GACATCTATGCTATGAAGTGTGAAGAGAGAGGCTTTATTGGCCCGAGGAGAGGTTTCA 420  
427 TTTTGTGAGGAGAGCGGAACTATTATCTCGAAGCACAAGCCCTGCGATCCCCCAATTA 486  
421 TTTTGTGAGGAGAGCGGAACTATTATCTCGAAGCACAAGCCCTGCGATCCCCCAATTA 480  
487 CAGTATGCTTTCCAGGACAAAATCACTTTTATCTGTCATGGAATATCAGCCTGGAGGG 546  
481 CAGTATGCTTTCCAGGACAAAATCACTTTTATCTGTCATGGAATATCAGCCTGGAGGG 540

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QY 547 GACTTGTCTGACATTTTGAATAGATATAGAGACAGTTAGATGAACCTGATACAGTTT 606
Db 541 GACTTGTCTGACATTTTGAATAGATATAGAGACAGTTAGATGAACCTGATACAGTTT 600
QY 607 TACCTAGCTGAGCTGATTTTGGCTGTTTACAGCGCTTCATCTGATGGGATACGTCATCGA 666
Db 601 TACCTAGCTGAGCTGATTTTGGCTGTTTACAGCGCTTCATCTGATGGGATACGTCATCGA 660
QY 667 GACATCAAGCTGAGAACATTTCTGTTGACCGGACAGGACACATCAAGCTGGTGATTTT 726
Db 661 GACATCAAGCTGAGAACATTTCTGTTGACCGGACAGGACACATCAAGCTGGTGATTTT 720
QY 727 GGATCTCGCGGAAATGAATTCAAACAGATGCTGAATGCAAACTCCGATTTGGGACC 786
Db 721 GGATCTCGCGGAAATGAATTCAAACAGATGCTGAATGCAAACTCCGATTTGGGACC 780
QY 787 CCAGATTACATGCTCTGCTGAGTCTGACTGTGATGAACGGGGATGAAAAAGGCACCTAC 846
Db 781 CCAGATTACATGCTCTGCTGAGTCTGACTGTGATGAACGGGGATGAAAAAGGCACCTAC 840
QY 847 GGCTGTGACTGTGACTGCTGCTGAGTGGGCTGATTTCCCTATGAGATGATTTATGGAGA 906
Db 841 GGCTGTGACTGTGACTGCTGCTGAGTGGGCTGATTTCCCTATGAGATGATTTATGGAGA 900
QY 907 TCCGCCCTTCGAGAGGAACTCTGCGCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966
Db 901 TCCGCCCTTCGAGAGGAACTCTGCGCAGAACCTTCAATAACATTATGAATTTCCAGCGG 960
QY 967 TTTTGTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGTGATCTGATTCAAAGC 1026
Db 961 TTTTGTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGTGATCTGATTCAAAGC 1020
QY 1027 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTGTGCTGCCATCTCTTCTTC 1086
Db 1021 TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTGTGCTGCCATCTCTTCTTC 1080
QY 1087 TCTAAAATTGACTGTGAACAACTTCGTAATCTCTCTCCCTCCCTTCGTTCCACCTCAAG 1146
Db 1081 TCTAAAATTGACTGTGAACAACTTCGTAATCTCTCTCCCTCCCTTCGTTCCACCTCAAG 1140
QY 1147 TCCGAGATGACACTCCAAATTTGATGAACAGAGAGAAATTCGTGGGTTTCATCCTCT 1206
Db 1141 TCTGACGATGACACTCCAAATTTGATGAACAGAGAGAAATTCGTGGGTTTCATCCTCT 1200
QY 1207 CCGTGCCAGCTGACCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGGTTTTCG 1266
Db 1201 CCGTGCCAGCTGACCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGGTTTTCG 1260
QY 1267 TACAGCAAGGCACTGGGGATTTCTGTTAGATCTGAGTCTGTTGTGCGGCTCTGGACTCC 1326
Db 1261 TACAGCAAGGCACTGGGGATTTCTGTTAGATCTGAGTCTGTTGTGCGGCTCTGGACTCC 1320
QY 1327 CTTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTTACAAGAC 1386
Db 1321 CTTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTTACAAGAC 1380
QY 1387 TCTCAGGACAAGTGTCAAGGT 1409
Db 1381 TCTCAGGACAAGTGTCAAGAT 1403
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## RESULT 10

US-10-791-666-1

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; Sequence 1, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10791,666
; CURRENT FILING DATE: 2004-03-02
```

```
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6165
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-791-666-1
```

Query Match 92.3%; Score 1398.2; DB 18; Length 6165;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 7 ATGTTGAAGTTCAAATATATGAGCGCGGAATCTTTTGGATGCTGCTGCTGAACCAATT 66
Db 1 ATGTTGAAGTTCAAATATATGAGCGCGGAATCTTTTGGATGCTGCTGCTGAACCAATT 60
QY 67 GCCAACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCAA 126
Db 61 GCCAGCCGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCAA 120
QY 127 CAGCAGATGCTCTCTCTTCCGAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAA 186
Db 121 CAGCAGATGCTCTCTCTTCCGAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAA 180
QY 187 GAATGAGTCAAGCTGCTCTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCCGGAAGTAT 246
Db 181 GAATGAGTCAAGCTGCTCTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCCGGAAGTAT 240
QY 247 TCCGACACATAGCTGAGTTACAGGAGCTCCAGCCTTCGCAAGAGACTTCGAAGTCAGA 306
Db 241 TCCGACACATAGCTGAGTTACAGGAGCTCCAGCCTTCGCAAGAGACTTCGAAGTCAGA 300
QY 307 AGTCTTGTAGTTGTGCTCACTTTGCTGAAGTGCAGTGTGAAGAGAGAAAGCAACCGGG 366
Db 301 AGTCTTGTAGTTGTGCTCACTTTGCTGAAGTGCAGTGTGAAGAGAGAAAGCAACCGGG 360
QY 367 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATGCGCCAGAGAGAGGTTTCA 426
Db 361 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATGCGCCAGAGAGAGGTTTCA 420
QY 427 TTTTGTGAGAGAGAGCGGACATATTTATCTCGAAGCACAAGCCGTTGGATCCCCCAATTA 486
Db 421 TTTTGTGAGAGAGAGCGGACATATTTATCTCGAAGCACAAGCCGTTGGATCCCCCAATTA 480
QY 487 CAGTATGCCCTTTCCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCTCGAGGG 546
Db 481 CAGTATGCCCTTTCCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCTCGAGGG 540
QY 547 GACTTCTGCTCACTTTTGAATAGATATAGGACCAAGTTAGATGAAGAAACCTGATACAGTTT 606
Db 541 GACTTCTGCTCACTTTTGAATAGATATAGGACCAAGTTAGATGAAGAAACCTGATACAGTTT 600
QY 607 TACCTAGCTGAGCTGATTTTGGCTGTTTACAGCGTTTCATCTGATGGATACGTCATCGA 666
Db 601 TACCTAGCTGAGCTGATTTTGGCTGTTTACAGCGTTTCATCTGATGGATACGTCATCGA 660
QY 667 GACATCAAGCTGAGAACATTTCTGTTGACCGCAGCAGGACACATCAAGCTGGTGATTTT 726
Db 661 GACATCAAGCTGAGAACATTTCTGTTGACCGCAGCAGGACACATCAAGCTGGTGATTTT 720
QY 727 GGATCTCGCGGAAATGAATTCAAACAGATGCTGAATGCAAACTCCGATTTGGGACC 786
Db 721 GGATCTCGCGGAAATGAATTCAAACAGATGCTGAATGCAAACTCCGATTTGGGACC 780
QY 787 CCAGATTACATGCTCTGCTGAGTCTGACTGTGATGAACGGGGATGAAAAAGGCACCTAC 846
Db 781 CCAGATTACATGCTCTGCTGAGTCTGACTGTGATGAACGGGGATGAAAAAGGCACCTAC 840
QY 847 GGCTGTGACTGTGACTGCTGCTGAGTGGGCTGATTTCCCTATGAGATGATTTATGGAGA 906
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Db      841  |||||GGCCTGGAGTGTGACTGGTGGTCACTGGGCGTGAATTCCTATGAGATGAATTAATGGAGA 900
Qy      907  TCCCCCTTCGACAGAGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 966
Db      901  TCCCCCTTCGACAGAGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 960
Qy      967  TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTTCTTGATCTGATTTCAAAAGC 1026
Db      961  TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTTCTTGATCTGATTTCAAAAGC 1020
Qy      1027  TTGTTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTGTGCGCAATCCTTTCTTC 1086
Db      1021  TTGTTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTGTGCGCAATCCTTTCTTC 1080
Qy      1087  TCTAAATTTGACTTGAACCAACATTTGTAACCTCTCCCTCCCTTCGTTCCACCTCAAG 1146
Db      1081  TCTAAATTTGACTTGAACCAACATTTGTAACCTCTCCCTCCCTTCGTTCCACCTCAAG 1140
Qy      1147  TCCGACGATGACACCTCCAAATTTTGATGAACCAAGAGAATTCGTGGGTTTCATCCTCT 1206
Db      1141  TCTGACGATGACACCTCCAAATTTTGATGAACCAAGAGAATTCGTGGGTTTCATCCTCT 1200
Qy      1207  CCGTCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTTCG 1266
Db      1201  CCGTCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTTCG 1260
Qy      1267  TACAGCAAGCACTGGGGATTTCTTGTAGATCTGAGTCTGTTGTCGGTCTGGAATCC 1326
Db      1261  TACAGCAAGCACTGGGGATTTCTTGTAGATCTGAGTCTGTTGTCGGTCTGGAATCC 1320
Qy      1327  CTGCAAGACTAGCTCCATGGAAGAAATCTCTCATCAAAAGCAAGAGCTACCAAGAC 1386
Db      1321  CCGTCCAGCACTAGCTCCATGGAAGAAATCTCTCATCAAAAGCAAGAGCTACCAAGAC 1380
Qy      1387  TCTCAGCAAGTGTCAAGGT 1409
Db      1381  TCTCAGCAAGTGTCAAGAT 1403
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RESULT 11
US-10-017-216-1
; Sequence 1, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPLELLER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1 Human Myotonic Dystrophy Type Prod
; FILE REFERENCE: 10147-57U1
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-216-1
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Query Match 92.3%; Score 1397.8; DB 13; Length 6574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Qy      1  GGGAGATGTTGAAGTTCAAAATATGGAGCGCGGAATCCTTTGATGCTGCTGCTGAA 60
Db      13  GGGAGATGTTGAAGTTCAAAATATGGAGCGCGGAATCCTTTGATGCTGCTGCTGAA 72
Qy      61  CCCATTGCCAACCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCCACCTTTATG 120
Db      73  CCCATTGCCAGCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCCACCTTTATG 132
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Qy      121  ACTCAACACAGAGATGTCTCTCTTTCCGAGAAAGGATATTAGATGCCCTCTTTGTCTC 180
Db      133  ACTCAACACAGAGATGTCTCTCTTTCCGAGAAAGGATATTAGATGCCCTCTTTGTCTC 192
Qy      181  TTTGAAGATGCACTGAGCTGCTCTCTGATGAAGATTAAAGCAGTGAAGCACTTTGTCGG 240
Db      193  TTTGAAGATGCACTGAGCTGCTCTCTGATGAAGATTAAAGCAGTGAAGCACTTTGTCGG 252
Qy      241  AAGTATTCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTCGGCAAGAGCTTCGAA 300
Db      253  AAGTATTCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTCGGCAAGAGCTTCGAA 312
Qy      301  GTCAGAAAGTCTTGTAGTTGTGCTCACTTTGTGAAGTGCAGGTGTAAGAGAAAGCA 360
Db      313  GTCAGAAAGTCTTGTAGTTGTGCTCACTTTGTGAAGTGCAGGTGTAAGAGAAAGCA 372
Qy      361  ACCGGGGACATCTATGCTATGAAGTGAAGAGAAAGGCTTTATTTGGCCCAAGGAGCAG 420
Db      373  ACCGGGGACATCTATGCTATGAAGTGAAGAGAAAGGCTTTATTTGGCCCAAGGAGCAG 432
Qy      421  GTTTTCATTTTTCAGGAAGAGCGGAACATATTATCTCGAAGCAACAAGCCCGTGGATCCCC 480
Db      433  GTTTTCATTTTTCAGGAAGAGCGGAACATATTATCTCGAAGCAACAAGCCCGTGGATCCCC 492
Qy      481  CAATTAACATATGCTCTTTCAGGAACAAATACCTTTATCTGCTCATGGAATATCAGCCT 540
Db      493  CAATTAACATATGCTCTTTCAGGAACAAATACCTTTATCTGCTCATGGAATATCAGCCT 552
Qy      541  GGAGGGGACCTTGTGCTCACTTTTGAATAGATATGAGGACAGTTAGATGAANAACCTGATA 600
Db      553  GGAGGGGACCTTGTGCTCACTTTTGAATAGATATGAGGACAGTTAGATGAANAACCTGATA 612
Qy      601  CAGTTTTCCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGATACGTG 660
Db      613  CAGTTTTCCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGATACGTG 672
Qy      661  CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 720
Db      673  CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 732
Qy      721  GATTTTGGATCTGCGCGGAAATGAATTCAAACAGATGGTGAATGCCAAACTCCCGATT 780
Db      733  GATTTTGGATCTGCGCGGAAATGAATTCAAACAGATGGTGAATGCCAAACTCCCGATT 792
Qy      781  GGGACCCACAGATTACATGCTCTCTGAAGTGTGACTGTGATGAACGGGATGGAAGGC 840
Db      793  GGGACCCACAGATTACATGCTCTCTGAAGTGTGACTGTGATGAACGGGATGGAAGGC 852
Qy      841  ACCTACGGCTGGAAGTGTGCTGAGTGGGCTGAGTGGGCTGATTTGCCCTATGAGATGATTAT 900
Db      853  ACCTACGGCTGGAAGTGTGCTGAGTGGGCTGAGTGGGCTGATTTGCCCTATGAGATGATTAT 912
Qy      901  GGGAGATCCCTTTCGACAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTTC 960
Db      913  GGGAGATCCCTTTCGACAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTTC 972
Qy      961  CAGCGGTTTTTGAAATTTCCAGATGACCCCAAGTGAGCAGTGAATTTCTTGATCTGATT 1020
Db      973  CAGCGGTTTTTGAAATTTCCAGATGACCCCAAGTGAGCAGTGAATTTCTTGATCTGATT 1032
Qy      1021  CAAAGCTTCTTGTGGCGCCAGAAAGAGAGACTGAAGTTTGAAGGCTCTTTGCTGCCATCCT 1080
Db      1033  CAAAGCTTCTTGTGGCGCCAGAAAGAGAGACTGAAGTTTGAAGGCTCTTTGCTGCCATCCT 1092
Qy      1081  TTCTTCTCTAAATTTGACTGGAAACAACTTCGTAACCTCTCTCCCTCCCTTGTGTTCCACC 1140
Db      1093  TTCTTCTCTAAATTTGACTGGAAACAACTTCGTAACCTCTCTCCCTCCCTTGTGTTCCACC 1152
Qy      1141  CTCAGTCCGAGTGAACACCTCCCAATTTTGTGACCAAGAGAAAGAAATTCGTGGGTTTCA 1200
Db      1153  CTCAGTCCGAGTGAACACCTCCCAATTTTGTGACCAAGAGAAAGAAATTCGTGGGTTTCA 1212
Qy      1201  TCCTCTCCGTCGACGTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGG 1260
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Db 1213 TCCTCTCGTCCAGCTGAGCCCTCAGGCTTCTCGGTGAAGAACTCGCCGTTGTGGG 1272  
Qy 1261 TTTCGTACAGACAGGCACTGGGATCTTGGTAGATCTGAGTCTGTGTGTGGGTCTG 1320  
Db 1273 TTTCGTACAGACAGGCACTGGGATCTTGGTAGATCTGAGTCTGTGTGTGGGTCTG 1332  
Qy 1321 GACTCCCTCCAGACTAGCTCCATGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
Db 1333 GACTCCCTCCAGACTAGCTCCATGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1392  
Qy 1381 CAAGACTCTCAGGACAAAGTGTCAAGGT 1409  
Db 1393 CAAGACTCTCAGGACAAAGTGTCAAGAT 1421

RESULT 12  
US-10-325-430-10  
; Sequence 10, Application US/10325430  
; Publication No. US2003015325A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Rosenfeld, Julie Beth  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,  
; TITLE OF INVENTION: 32838, 336 and 52908  
; FILE REFERENCE: ME101-294PIRNM  
; CURRENT APPLICATION NUMBER: US/10/325,430  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/341,953  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 6574  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-325-430-10

Query Match 92.3%; Score 1397.8; DB 16; Length 6574;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGAGATGTTGAAGTTCAATATGGAGCGGAATCCTTTGGATGCTGTGCTGTGAA 60  
Db 13 GGGAGATGTTGAAGTTCAATATGGAGCGGAATCCTTTGGATGCTGTGCTGTGAA 72  
Qy 61 CCCATTGCCAACCGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCACTTTATG 120  
Db 73 CCCATTGCCAGCCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCACTTTATG 132  
Qy 121 ACTCAAGAGATGCTCTCTTTCCGAGAGGGATATAGATGCTCTTTGTTCTC 180  
Db 133 ACTCAAGAGATGCTCTCTTTCCGAGAGGGATATAGATGCTCTTTGTTCTC 192  
Qy 181 TTGAAGAAATGCACTGAGCTGCTCTGATCAAGATTAAAGCACGTCAGCACTTTGTCGG 240  
Db 193 TTGAAGAAATGCACTGAGCTGCTCTGATCAAGATTAAAGCACGTCAGCACTTTGTCGG 252  
Qy 241 AAGTATTCGACACCAATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAAAGGACTTCGAA 300  
Db 253 AAGTATTCGACACCAATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAAAGGACTTCGAA 312  
Qy 301 GTCAAGATCTTGTAGTTGTGTCCTTTGCTGAGTGCAGTGTGTAAGAGAAAGCA 360  
Db 313 GTCAAGATCTTGTAGTTGTGTCCTTTGCTGAGTGCAGTGTGTAAGAGAAAGCA 372  
Qy 361 ACCGGGACATCTATGCTATGAAGTGTATGAAGAGGCTTTATTGGCCACAGGAGCA 420  
Db 373 ACCGGGACATCTATGCTATGAAGTGTATGAAGAGGCTTTATTGGCCACAGGAGCA 432  
Qy 421 GTTTTCATTTTGGAGGAGCGGAAATATATCTCGAAGCACAAAGCCGTCGATCCCC 480

Db 433 GTTTTCATTTTGGAGGAGCGGAACATATATCTCGAAGCACAAAGCCGTCGATCCCC 492  
Qy 481 CAATTAAGATATGCTTTTCAGGACAAAATACCTTTTATCTGGTCAATGAATATCAGCCT 540  
Db 493 CAATTAAGATATGCTTTTCAGGACAAAATACCTTTTATCTGGTCAATGAATATCAGCCT 552  
Qy 541 GGAGGGGACTTGTGTGTCACCTTTTGAATAGATATGAGGACAGTTAGATGAAAACCTGATA 600  
Db 553 GGAGGGGACTTGTGTGTCACCTTTTGAATAGATATGAGGACAGTTAGATGAAAACCTGATA 612  
Qy 601 CAGTTTACCTAGCTAGCTGAGTGTATTTTGGCTGTTTTCAGAGGTTTTCATCTGATGGATACGTG 660  
Db 613 CAGTTTACCTAGCTAGCTGAGTGTATTTTGGCTGTTTTCAGAGGTTTTCATCTGATGGATACGTG 672  
Qy 661 CATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 720  
Db 673 CATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 732  
Qy 721 GATTTTGGATCTGCCCGGAAATGAATTCAAAACAAGATGTTGAATGCCAAACTCCCGATT 780  
Db 733 GATTTTGGATCTGCCCGGAAATGAATTCAAAACAAGATGTTGAATGCCAAACTCCCGATT 792  
Qy 781 GGGACCCAGATTAACATGCTCTCTGAAGTGTGCTGATGAACCGGGATGAAAAGGC 840  
Db 793 GGGACCCAGATTAACATGCTCTCTGAAGTGTGCTGATGAACCGGGATGAAAAGGC 852  
Qy 841 ACCTACGGCTGAGTGTGCTGAGTGGGCTGATGCGGCTGATGCGCTATGAGATTTAT 900  
Db 853 ACCTACGGCTGAGTGTGCTGAGTGGGCTGATGCGGCTGATGCGCTATGAGATTTAT 912  
Qy 901 GGGAGATCCCCCTTCGAGAGGAACTCTGCGAGAACCTTCAATAACATTAATGAATTC 960  
Db 913 GGGAGATCCCCCTTCGAGAGGAACTCTGCGAGAACCTTCAATAACATTAATGAATTC 972  
Qy 961 CAGCGGTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAATTTCTGATCTGATT 1020  
Db 973 CAGCGGTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAATTTCTGATCTGATT 1032  
Qy 1021 CAAAGCTTGTGTCGGCCAGAGAGACATGAACTTTGAAAGTCTTTGCTGCCATCCT 1080  
Db 1033 CAAAGCTTGTGTCGGCCAGAGAGACATGAACTTTGAAAGTCTTTGCTGCCATCCT 1092  
Qy 1081 TTCTTCTTAAATTTGACTGGAACTTCTGTAATCTCTCTCCCTCCCTTCTGTTCCACC 1140  
Db 1093 TTCTTCTTAAATTTGACTGGAACTTCTGTAATCTCTCTCCCTCCCTTCTGTTCCACC 1152  
Qy 1141 CTCAGTCCGAGATGACACCTTCAATTTTGAATGAACCGAGAGAAATTCGTGGGTTTCA 1200  
Db 1153 CTCAGTCCGAGATGACACCTTCAATTTTGAATGAACCGAGAGAAATTCGTGGGTTTCA 1212  
Qy 1201 TCCTCTCCGTCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTGTTGGG 1260  
Db 1213 TCCTCTCCGTCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTGTTGGG 1272  
Qy 1261 TTTTCGTACAGCAAGGCACTGGGATTTCTGGTAGATCTGAGTCTGTTGTCGGGCTG 1320  
Db 1273 TTTTCGTACAGCAAGGCACTGGGATTTCTGGTAGATCTGAGTCTGTTGTCGGGCTG 1332  
Qy 1321 GACTCCCTCCAGACTAGCTCCATGAAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
Db 1333 GACTCCCTCCAGACTAGCTCCATGAAAAGAACTTCTCATCAAAAGCAAGAGCTA 1392  
Qy 1381 CAAAGCTCTCAGGACAAAGTGTCAAGGT 1409  
Db 1393 CAAAGCTCTCAGGACAAAGTGTCAAGAT 1421

RESULT 13  
US-10-757-262-51  
; Sequence 51, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:



```

; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 43390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2538, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2153, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007PIRNONMIN
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR FILING DATE: 2004-01-14
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/458,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)...(6180)
US-10-757-262-51

Query Match      92.3%; Score 1397.8; DB 18; Length 6574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGAGATGTTGAAGTTCATATGAGCGCGGAATCCTTTGGATGCTGGTGTCTGAA 60
DB 13 GGGGAGATGTTGAAGTTCATATGAGCGCGGAATCCTTTGGATGCTGGTGTCTGAA 72
QY 61 CCATATGCCAACCGGGCTCCAGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATG 120
DB 73 CCATATGCCAGCGGGCTCCAGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATG 132
QY 121 ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATTAGATGCCCTTTTGTCTC 180
DB 133 ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATTAGATGCCCTTTTGTCTC 192
QY 181 TTTGAAGATGCGATGAGCTGCTCTGATCAAGATTAAAGCAGCTGAGCACTTTGTCGG 240
DB 193 TTTGAAGATGCGATGAGCTGCTCTGATCAAGATTAAAGCAGCTGAGCACTTTGTCGG 252
QY 241 AAGTATTTCCACACCACTAGCTGAGTTACAGAGCTCCAGAGCTTCGGCAAGAGACTTCGAA 300
DB 253 AAGTATTTCCACACCACTAGCTGAGTTACAGAGCTCCAGAGCTTCGGCAAGAGACTTCGAA 312
QY 301 GTCAGAGATCTTGTAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTGAAGAGAAAGCA 360
DB 1393 CAAGACTCTCAGGACAAGTGTCAAGAT 1421

313 GTCAGAAAGTCTTGTAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTGAAGAGAAAGCA 372
361 ACCGGGAGACATCTATGCTATGAAGTGTATGAAGAAGAGCTTTTATTTGGCCAGGAGCAG 420
373 ACCGGGAGACATCTATGCTATGAAGTGTATGAAGAAGAGCTTTTATTTGGCCAGGAGCAG 432
421 GTTTCATATTTTTCGAGGAAGCGGAACATATTTATCTCGAAGCAACAAGCCCGTGGATCCCC 480
433 GTTTCATATTTTTCGAGGAAGCGGAACATATTTATCTCGAAGCAACAAGCCCGTGGATCCCC 492
481 CAATTAAGTATGCTCTTCAGGACAAATATCACTTTATCTGCTCATGGAATATCAGCCT 540
493 CAATTAAGTATGCTCTTCAGGACAAATATCACTTTATCTGATGGAGGAATATCAGCCT 552
541 GGAGGGAGACTTGTGTCACATTTTGAATAGATATGAGGACCAAGTATAGATGAAGAACTGATA 600
553 GGAGGGAGACTTGTGTCACATTTTGAATAGATATGAGGACCAAGTATAGATGAAGAACTGATA 612
601 CAGTTTAACTAGCTGAGCTGATTTTGGCTGTTTTCACAGCGTTCATCTGATGGGATACGTG 660
613 CAGTTTAACTAGCTGAGCTGATTTTGGCTGTTTTCACAGCGTTCATCTGATGGGATACGTG 672
661 CATCGAGACATCAAGCTCAGAACATTTCTGTTGACCGGACAGGACACATCAAGCTGGTG 720
673 CATCGAGACATCAAGCTCAGAACATTTCTGTTGACCGGACAGGACACATCAAGCTGGTG 732
721 GATTTTGGATCTGCGCGGAATATGAATTTCAACAAGATGTTGAATGCAAACTCCCGATT 780
733 GATTTTGGATCTGCGCGGAATATGAATTTCAACAAGATGTTGAATGCAAACTCCCGATT 792
781 GGGACCCCAAGATTTACATGCTCTCTGAACTGCTGATGAACGGGATGGAAGAGGC 840
793 GGGACCCCAAGATTTACATGCTCTCTGAACTGCTGATGAACGGGATGGAAGAGGC 852
841 ACCTACGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
853 ACCTACGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912
901 GGGAGATCCCCCTTCGAGAGGAACTCTGCCAGAACTCTGCCAGAACTCTCAATTAACATTTT 960
913 GGGAGATCCCCCTTCGAGAGGAACTCTGCCAGAACTCTGCCAGAACTCTCAATTAACATTTT 972
961 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGCAGTGAATTTTCTGATCTGAT 1020
973 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGCAGTGAATTTTCTGATCTGAT 1032
1021 CAAAGCTTGTGTGCGGACAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCGCATCCT 1080
1033 CAAAGCTTGTGTGCGGACAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCGCATCCT 1092
1081 TTCTTCTTAAATTTGACCTGGAACAACTTCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1140
1093 TTCTTCTTAAATTTGACCTGGAACAACTTCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1152
1141 CTCAAGTCCGAGCAGATGACACCTCCAATTTTGAATGAACAGAGAGAAATTCGTGGTTTCA 1200
1153 CTCAAGTCCGAGCAGATGACACCTCCAATTTTGAATGAACAGAGAGAAATTCGTGGTTTCA 1212
1201 TCCTCTCCGTCAGCTGAGCCCTCAGGCTTCCTGGGTGAGAACTGCGGCTTTTGGGG 1260
1213 TCCTCTCCGTCAGCTGAGCCCTCAGGCTTCCTGGGTGAGAACTGCGGCTTTTGGGG 1272
1261 TTTTCGTACAGCAAGCAGCTGGGGATTTCTTGGTAGATCTGAGTCTGTTGCTGGGCTG 1320
1273 TTTTCGTACAGCAAGCAGCTGGGGATTTCTTGGTAGATCTGAGTCTGTTGCTGGGCTG 1332
1321 GACTCCCTGCCAAGACTAGCTCCATGGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380
1333 GACTCCCTGCCAAGACTAGCTCCATGGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1392
1381 CAAGACTCTCAGGACAAGTGTCAAGGT 1409
1393 CAAGACTCTCAGGACAAGTGTCAAGAT 1421
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RESULT 14  
US-10-017-216-3  
; Sequence 3, Application US/10017216  
; Publication No. US20020160483A1  
; GENERAL INFORMATION:  
; APPLICANT: KAPILLER-LIBERMAN, Rosana  
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prob  
; TITLE OF INVENTION: Kinase and Uses Therefor  
; FILE REFERENCE: 10147-57U1  
; CURRENT APPLICATION NUMBER: US/10/017,216  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/242,429  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 6159  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-017-216-3

Query Match 91.9%; Score 1391.8; DB 13; Length 6159;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1396; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	7	ATGTTGAAGTTCAAAATATGAGCGCGGAATCCCTTTGGATGCTGGTGTCTGTAACCAATT	66
Db	1	ATGTTGAAGTTCAAAATATGAGCGCGGAATCCCTTTGGATGCTGGTGTCTGTAACCAATT	60
Qy	67	GCCAAACGGGCTCCAGCTGAACTCTCTTCCAGGGGAACACCCCTTTATGACTCAA	126
Db	61	GCCAGCGGGCTCCAGCTGAACTCTCTTCCAGGGGAACACCCCTTTATGACTCAA	120
Qy	127	CAGCAGATGTCCTCTCTTCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGA	186
Db	121	CAGCAGATGTCCTCTCTTCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTGAA	180
Qy	187	GAATGAGTCAAGCTGCTCTGATGAAGTAATGAAGCACTGAGCACTTTGTCGGAAGTAT	246
Db	181	GAATGAGTCAAGCTGCTCTGATGAAGTAATGAAGCACTGAGCACTTTGTCGGAAGTAT	240
Qy	247	TCCGACACCATAGCTGAGTTACAGAGCTCCAGGCTTCGCAAGAGACTTCGAAGTCAGA	306
Db	241	TCCGACACCATAGCTGAGTTACAGAGCTCCAGGCTTCGCAAGAGACTTCGAAGTCAGA	300
Qy	307	AGTCTTGTAGTTGGTCTCACTTTGCTGAAGTGCAGGTGGTAAAGAGAAAGCAACCGGG	366
Db	301	AGTCTTGTAGTTGGTCTCACTTTGCTGAAGTGCAGGTGGTAAAGAGAAAGCAACCGGG	360
Qy	367	GACATCTATGCTATGAAGTATGAAGAAGGCTTTATGGCCAGGAGCAGGTTTCA	426
Db	361	GACATCTATGCTATGAAGTATGAAGAAGGCTTTATGGCCAGGAGCAGGTTTCA	420
Qy	427	TTTTTTCAGGAAGCGGAACATATTCTCGAAGCAAGCCGCTGGATCCCAATTA	486
Db	421	TTTTTTCAGGAAGCGGAACATATTCTCGAAGCAAGCCGCTGGATCCCAATTA	480
Qy	487	CAGTATGCCCTTCAGGACAAAATACCTTTATCTGCTATGGAATATCAGCCCTGGAGGG	546
Db	481	CAGTATGCCCTTCAGGACAAAATACCTTTATCTGCTATGGAATATCAGCCCTGGAGGG	540
Qy	547	GACTTGTCTGCTATTTGAATAGATAGAGACAGGTTAGATGAACCTGATACAGTTT	606
Db	541	GACTTGTCTGCTATTTGAATAGATAGAGACAGGTTAGATGAACCTGATACAGTTT	600
Qy	607	TACCTAGCTAGCTGATTTTGGCTGTTTACAGCGCTTCTATCTGATGGATACGTCATCGA	666
Db	601	TACCTAGCTAGCTGATTTTGGCTGTTTACAGCGCTTCTATCTGATGGATACGTCATCGA	660
Qy	667	GACATCAAGCTTGAGAACTTCTGTTTGAACCGACACGATCAAGCTGGTGGATTTT	726

661 GACATCAAGCCTGAGAAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 720  
727 GGATCTGCCGCGGAAATGAATTCAAAACAAGATGGTGAATGCCAAACTCCCGATTTGGAGCC 786  
721 GGATCTGCCGCGGAAATGAATTCAAAACAAGATGGTGAATGCCAAACTCCCGATTTGGAGCC 780  
787 CCAGATTACATGGCTCTCTGAAGTGTGACTGTGATGAACGGGGATGGAAAAGGCACCTAC 846  
781 CCAGATTACATGGCTCTCTGAAGTGTGACTGTGATGAACGGGGATGGAAAAGGCACCTAC 840  
847 GGCTGGACTGTGACTGTGGTGTGAGTGGCGTGTGATTCCTATCAGATGATTTATGGAGAGA 906  
841 GGCTGGACTGTGACTGTGGTGTGAGTGGCGTGTGATTCCTATCAGATGATTTATGGAGAGA 900  
907 TCCCCCTTTCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTTATGAATTTCCAGCGG 966  
901 TCCCCCTTTCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTTATGAATTTCCAGCGG 960  
967 TTTTTCGAAATTTCCAGATGACCCCAAGTTCAGCAGTGACTTTCTTCTGATCTGTATCAAGC 1026  
961 TTTTTCGAAATTTCCAGATGACCCCAAGTTCAGCAGTGAGTCTTTCTTCTGATCTGTATCAAGC 1020  
1027 TTCTTGTGGCGCCAGAAAGAGAGACTGAAAGTTTGAAGTCTTTTGTGCTGCCATCCTTTCTTC 1086  
1021 TTCTTGTGGCGCCAGAAAGAGAGACTGAAAGTTTGAAGTCTTTTGTGCTGCCATCCTTTCTTC 1080  
1087 TCTAAATTTGACTGGAAACAACATTCGTAATCTCTCTCCCTCCCTTCTGTTCCACCTCAAG 1146  
1081 TCTAAATTTGACTGGAAACAACATTCGTAATCTCTCTCCCTCCCTTCTGTTCCACCTCAAG 1140  
1147 TCCGACGATGACACCTCCAAATTTTGTATGAACAGAGAAATTCGTGGGTTTTCATCTCT 1206  
1141 TCTGACGATGACACCTCCAAATTTTGTATGAACAGAGAGATTCGTGGGTTTTCATCTCT 1200  
1207 CCGTCCAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGGTTTTCG 1266  
1201 CCGTCCAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGGTTTTCG 1260  
1267 TACAGCAAGCCTGCGGATTTCTGATAGTCTGATAGTCTGTTGTCGGTCTGGACTCC 1326  
1261 TACAGCAAGCCTGCGGATTTCTGATAGTCTGATAGTCTGTTGTCGGTCTGGACTCC 1320  
1327 CTGCCCCAGCTAGCTCCATGAAAAAGAACTTCTCATCAAAAGCAAGAGCTTACAAGC 1386  
1321 CTGCCCCAGCTAGCTCCATGAAAAAGAACTTCTCATCAAAAGCAAGAGCTTACAAGC 1380  
1387 TCTCAGCAAGTGTCAAGGT 1409  
1381 TCTCAGCAAGTGTCAAGAT 1403

RESULT 15  
US-10-325-430-11  
; Sequence 11, Application US/10325430  
; Publication No. US20030153525A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: Silesio-Santiago, Immaculada  
; APPLICANT: Rosenfeld, Julie Beth  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,  
; TITLE OF INVENTION: 32838,336 and 52908  
; FILE REFERENCE: MPI01-294P1RM  
; CURRENT APPLICATION NUMBER: US/10/325,430  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/341,953  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 6162  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)... (6162)
US-10-325-430-11

Query Match      91.98; Score 1391.8; DB 16; Length 6162;
Best Local Similarity 99.54; Pred. No. 0;
Matches 1396; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 7 ATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATT 66
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Db 1 ATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATT 60

QY 67 GCCAACCGGGCCCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCCACCTTTATGACTCAA 126
   |||||
Db 61 GCCAGCGGGCCCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCCACCTTTATGACTCAA 120

QY 127 CAGCAGATGTCCTCTCTTTCCAGAAAGGATATAGATGCCCTCTTTGTTCTCTTTGAA 186
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Db 121 CAGCAGATGTCCTCTCTTTCCAGAAAGGATATAGATGCCCTCTTTGTTCTCTTTGAA 180

QY 187 GAATGCAGTCAGGCTGCTCTGATGAAGATTAAAGCAGTGAGCAACTTTGTCGGGAAGTAT 246
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Db 181 GAATGCAGTCAGGCTGCTCTGATGAAGATTAAAGCAGTGAGCAACTTTGTCGGGAAGTAT 240

QY 247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTTCCGCAAGGACTTTCGAAGTCAGA 306
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Db 241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTTCCGCAAGGACTTTCGAAGTCAGA 300

QY 307 AGTCTTTGAGTTGTTGTTCTCTTTGTAAGTGAGTGAGTGTAAGAGAAAGCAACCGGG 366
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Db 301 AGTCTTTGAGTTGTTGTTCTCTTTGTAAGTGAGTGAGTGTAAGAGAAAGCAACCGGG 360

QY 367 GACATCTATCTATGAAGTGATGAAGAAAGGCTTTATTGGCCAGAGGAGGTTTCA 426
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Db 361 GACATCTATCTATGAAGTGATGAAGAAAGGCTTTATTGGCCAGAGGAGGTTTCA 420

QY 427 TTTTTCAGGAAGAGCGGAAACATATTATCTCGAAGCACAGCCCGTGGAATCCCCCAATTA 486
   |||||
Db 421 TTTTTCAGGAAGAGCGGAAACATATTATCTCGAAGCACAGCCCGTGGAATCCCCCAATTA 480

QY 487 CAGTATGCCCTTCAGGACAAAATCACTTTTATCTGGTCAATGAATATCAGCCTGGAGGG 546
   |||||
Db 481 CAGTATGCCCTTCAGGACAAAATCACTTTTATCTGGTCAATGAATATCAGCCTGGAGGG 540

QY 547 GACTTCTGTCTCACTTTTGAATGATATGAGGACCAAGTATGATGAAACCTGATACAGTTT 606
   |||||
Db 541 GACTTCTGTCTCACTTTTGAATGATATGAGGACCAAGTATGATGAAACCTGATACAGTTT 600

QY 607 TACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCGTTTCATCTGATGGATACGTGCAATCGA 666
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Db 601 TACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCGTTTCATCTGATGGATACGTGCAATCGA 660

QY 667 GACATCAAGCCTCAGAACCAATTCCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTT 726
   |||||
Db 661 GACATCAAGCCTCAGAACCAATTCCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTT 720

QY 727 GGATCTGCCCGGAAATGATTTCAACACAGATGGTGAATGCCAACTCCCGATTGGGACC 786
   |||||
Db 721 GGATCTGCCCGGAAATGATTTCAACACAGATGGTGAATGCCAACTCCCGATTGGGACC 780

QY 787 CCAGATTACATGGCTCTGTAAGTGCTGACTGATGAACGGGGATGGAAAGGCACTTAC 846
   |||||
Db 781 CCAGATTACATGGCTCTGTAAGTGCTGACTGATGNAACGGGGATGGAAAGGCACTTAC 840

QY 847 GGCTTGAGCTGTGACTGGTGGTCAAGTGGGCGTGAATGCCCTATCAGATGATTTATGGGAGA 906
   |||||
Db 841 GGCTTGAGCTGTGACTGGTGGTCAAGTGGGCGTGAATGCCCTATCAGATGATTTATGGGAGA 900

QY 907 TCCCCCTTCGACAGGGGAACTCTGCCAGAACCTTCAATAACATTATGATTTCCAGCGG 966
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Db 901 TCCCCCTTCGACAGGGGAACTCTGCCAGAACCTTCAATAACATTATGATTTCCAGCGG 960
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 07:56:21 ; Search time 267.502 Seconds  
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9267.079 Million cell updates/sec

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1515	100.0	1515	4	US-09-804-471A-1
2	1515	100.0	1515	4	US-10-238-709-1
3	1398.2	92.3	5877	4	US-10-028-946-3
4	1398.2	92.3	6165	4	US-10-028-946-1
5	963.2	63.6	2162	4	US-09-774-528-419
6	760.8	50.2	1133	4	US-09-916-204-1
7	760.8	50.2	1133	4	US-10-282-048-1
8	234.6	15.5	2433	4	US-09-949-016-2640
9	225.6	14.9	2726	2	US-08-422-699A-12
10	225.6	14.9	2726	2	US-08-422-706B-12
11	218.8	14.4	2511	2	US-08-422-699A-8
12	218.8	14.4	2511	2	US-08-422-706B-8
13	218.4	14.4	3182	1	US-08-484-044-11
14	216.2	14.3	174493	4	US-09-804-471A-3
15	216.2	14.3	174493	4	US-10-238-709-3
16	194	12.8	2706	2	US-08-630-822A-61
17	194	12.8	2706	2	US-09-005-069-61
18	194	12.8	2706	3	US-09-171-156A-20
19	194	12.8	2706	4	US-09-004-730A-20
20	194	12.8	2706	4	US-08-981-799A-20
21	186	12.3	4363	2	US-08-685-576-5
22	184.4	12.2	4848	4	US-09-976-594-295
23	178.8	11.8	48763	4	US-09-916-204-3
24	178.8	11.8	48763	4	US-10-282-048-3
25	175.4	11.6	4065	4	US-09-016-434-1105
26	175.4	11.6	4739	3	US-08-685-871-1
27	171.6	11.3	5053	2	US-08-685-576-2

28	156.4	10.3	3323	2	US-08-422-699A-10	Sequence 10, Appl
29	156.4	10.3	3323	2	US-08-422-706B-10	Sequence 10, Appl
30	125.8	8.3	3155	3	US-09-442-100-7	Sequence 7, Appl
31	125.8	8.3	3155	4	US-08-939-106-7	Sequence 7, Appl
32	125.8	8.3	3155	4	US-09-442-102-7	Sequence 7, Appl
33	125.4	8.3	1498	3	US-09-509-902A-6	Sequence 6, Appl
34	125.4	8.3	1961	3	US-09-509-902A-15	Sequence 15, Appl
35	125.4	8.3	5276	4	US-09-233-857-2	Sequence 2, Appl
36	121	8.0	3018	2	US-08-860-150-6	Sequence 6, Appl
37	121	8.0	3018	2	US-09-338-132-6	Sequence 6, Appl
38	114.6	7.6	1935	2	US-08-878-989-11	Sequence 11, Appl
39	114.6	7.6	1935	3	US-09-272-796-11	Sequence 11, Appl
40	113	7.5	3213	3	US-09-442-100-5	Sequence 5, Appl
41	113	7.5	3213	4	US-08-939-106-5	Sequence 5, Appl
42	113	7.5	3213	4	US-09-442-102-5	Sequence 5, Appl
43	110.4	7.3	1251	4	US-09-248-796A-4400	Sequence 4400, Ap
44	108	7.1	2160	3	US-09-588-256-1	Sequence 1, Appl
45	104.6	6.9	5720	3	US-09-442-100-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-09-804-471A-1  
; Sequence 1, Application US/09804471A  
; Patent No. 6479269  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164  
; CURRENT APPLICATION NUMBER: US/09/804,471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Human  
US-09-804-471A-1

Query Match	100.0%	Score 1515;	DB 4;	Length 1515;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1515;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	GGGAGAGTGTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA	60	
Db	1	GGGAGAGTGTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA	60	
QY	61	CCCATGGCCACCGGCGCTCCAGGCTGAATCTTTCTCCAGGGGAACACCCCTTTATG	120	
Db	61	CCCATGGCCACCGGCGCTCCAGGCTGAATCTTTCTCCAGGGGAACACCCCTTTATG	120	
QY	121	ACTCAACAGCAGATGCTCTCTTTCCGAGAGGATATTAGATGCCCTTTTGTCTC	180	
Db	121	ACTCAACAGCAGATGCTCTCTTTCCGAGAGGATATTAGATGCCCTTTTGTCTC	180	
QY	181	TTTGAAGAATGCAAGTCAGCTGCTCTGTATGAAGATTAAAGCAGCTGAGCACTTTGTCGG	240	
Db	181	TTTGAAGAATGCAAGTCAGCTGCTCTGTATGAAGATTAAAGCAGCTGAGCACTTTGTCGG	240	
QY	241	AGTATTCGACACCACTAGCTAGTTACAGGAGCTCCAGCTTCGGCAAGGACTTCGAA	300	
Db	241	AGTATTCGACACCACTAGCTAGTTACAGGAGCTCCAGCTTCGGCAAGGACTTCGAA	300	
QY	301	GTGAGAGTCTTGTAGTTGTGCTCACTTTGCTGAAGTGCAGTGTGAAGAGCA	360	
Db	301	GTGAGAGTCTTGTAGTTGTGCTCACTTTGCTGAAGTGCAGTGTGAAGAGCA	360	
QY	361	ACGGGGACATCTATGCTATGAAGTGAAGAGGCTTTATTTGGCCAGGAGCAG	420	



Qy	661	CATCGAGCATCAAGCCTGAGAA	CATTCTCGTTGACCGCACAGACACATCAAGCTGGT	720
Db	661	CATCGAGCATCAAGCCTGAGAA	CATTCTCGTTGACCGCACAGACACATCAAGCTGGT	720
Qy	721	GATTTTGGATCTCGCGGAAATGA	TTCAAAACAAGATGGTGAATGCCAAACTCCCGATT	780
Db	721	GATTTTGGATCTCGCGGAAATGA	TTCAAAACAAGATGGTGAATGCCAAACTCCCGATT	780
Qy	781	GGGACCCAGATTACATGGCTCTG	AAGTGTGATGAACGGGGATGGAAAAAGGC	840
Db	781	GGGACCCAGATTACATGGCTCTG	AAGTGTGATGAACGGGGATGGAAAAAGGC	840
Qy	841	ACCTACGGCCTGGACTGTGAC	TGGTGGTCACTGGCGGTGATGTCCTATGAGATGATTAT	900
Db	841	ACCTACGGCCTGGACTGTGAC	TGGTGGTCACTGGCGGTGATGTCCTATGAGATGATTAT	900
Qy	901	GGGAGATCCCCCTTCGCAGAG	GGGAACCTCTGCCAGAACCTTCAATAACATTATCAATTC	960
Db	901	GGGAGATCCCCCTTCGCAGAG	GGGAACCTCTGCCAGAACCTTCAATAACATTATCAATTC	960
Qy	961	CAGCGGTTTTGAAATTTCCAG	ATGACCCCAAAGTAGAGTAGCTTTCTTGATCTGATT	1020
Db	961	CAGCGGTTTTGAAATTTCCAG	ATGACCCCAAAGTAGAGTAGCTTTCTTGATCTGATT	1020
Qy	1021	CAAAAGCTTGTGTCGGCCG	AAAGAGAGACTGAAGTTGAAAGTCTTTGCTGCGCATCCT	1080
Db	1021	CAAAAGCTTGTGTCGGCCG	AAAGAGAGACTGAAGTTGAAAGTCTTTGCTGCGCATCCT	1080
Qy	1081	TTCTTCTCTAAAATTTGACT	GGAACAAATTCGTAACTCTCTCTCCCTTCGTTCCCAACC	1140
Db	1081	TTCTTCTCTAAAATTTGACT	GGAACAAATTCGTAACTCTCTCTCCCTTCGTTCCCAACC	1140
Qy	1141	CTCAAGTCCGACGATGAC	ACTCCAAATTTTGATGAAACAGAGAGAATTCGTGGGTTTCA	1200
Db	1141	CTCAAGTCCGACGATGAC	ACTCCAAATTTTGATGAAACAGAGAGAATTCGTGGGTTTCA	1200
Qy	1201	TCCTCTCGGTGCCAGCTGAG	CCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGCGGG	1260
Db	1201	TCCTCTCGGTGCCAGCTGAG	CCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGCGGG	1260
Qy	1261	TTTTTCGTACAGCAAGGCA	CTGGGATTCCTTGGTAGATCTGAGTCTGTGTGTCGGGCTG	1320
Db	1261	TTTTTCGTACAGCAAGGCA	CTGGGATTCCTTGGTAGATCTGAGTCTGTGTGTCGGGCTG	1320
Qy	1321	GACTCCCTTCGCAAGACTAG	CTCCATGGAAAAAGAAATTCATCAATAAAGCAAGAGCTA	1380
Db	1321	GACTCCCTTCGCAAGACTAG	CTCCATGGAAAAAGAAATTCATCAATAAAGCAAGAGCTA	1380
Qy	1381	CAGACTCTCAGGACAGTGTCA	CAAGGTATTTATTTCCGACGCGCGCTCTTCCTTTC	1440
Db	1381	CAGACTCTCAGGACAGTGTCA	CAAGGTATTTATTTCCGACGCGCGCTCTTCCTTTC	1440
Qy	1441	TCCAGGATCTCCCGTCCGTAT	ATGCCAAAGGATCCGCGCGCGCGCTCTTCCTTTC	1500
Db	1441	TCCAGGATCTCCCGTCCGTAT	ATGCCAAAGGATCCGCGCGCGCGCTCTTCCTTTC	1500
Qy	1501	GCGCCTGTATCCGTA	1515	
Db	1501	GCGCCTGTATCCGTA	1515	

RESULT 3  
US-10-028-946-3  
; Sequence 3, Application US/10028946  
; Patent No. 6734009  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Eridde, Carl Johan  
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028.946

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; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-028-946-3

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Query Match	92.3%	Score 1398.2	DB 4	Length 5877
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1400	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	7	ATGTTGAAGTTCAAATATGAGCGCGAATCTTTTGGATGCTGCTGCTGCTGAACCCATT	66	
Db	1	ATGTTGAAGTTCAAATATGAGCGCGAATCTTTTGGATGCTGCTGCTGCTGAACCCATT	60	
Qy	67	GCCAAACGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATGACTCAA	126	
Db	61	GCCAGCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATGACTCAA	120	
Qy	127	CAGCAGATGCTCCTCTTTCCGAGAGGGAATATTAGATGCCCTCTTTGTTCTCTTTGAA	186	
Db	121	CAGCAGATGCTCCTCTTTCCGAGAGGGAATATTAGATGCCCTCTTTGTTCTCTTTGAA	180	
Qy	187	GAATGCAGTCAGCCTGCTCTGATGAAGATTAAAGCATGTAGCAACTTTGTCGGGAAGTAT	246	
Db	181	GAATGCAGTCAGCCTGCTCTGATGAAGATTAAAGCATGTAGCAACTTTGTCGGGAAGTAT	240	
Qy	247	TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAGTCCAGA	306	
Db	241	TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAGTCCAGA	300	
Qy	307	AGTCTTTGAGTTGTGCTCACTTTTGCTGAAGTCAGTGGTAAAGAGAGAAAGCAACCGGG	366	
Db	301	AGTCTTTGAGTTGTGCTCACTTTTGCTGAAGTCAGTGGTAAAGAGAGAAAGCAACCGGG	360	
Qy	367	GACATCTATGCTATGAAGTGATGAAGAAGAGGCTTTATTGGCCCAAGGAGGTTTCA	426	
Db	361	GACATCTATGCTATGAAGTGATGAAGAAGAGGCTTTATTGGCCCAAGGAGGTTTCA	420	
Qy	427	TTTTTTTGAAGAGAGCGGAACATATTATCTCGAAGACCAAGCCCGTGGATCCCCCAATTA	486	
Db	421	TTTTTTTGAAGAGAGCGGAACATATTATCTCGAAGACCAAGCCCGTGGATCCCCCAATTA	480	
Qy	487	CAGTATGCCCTTTCAGGACAAAATACACCTTTATCTGTCATGGAATATCAGCCTGGAGGG	546	
Db	481	CAGTATGCCCTTTCAGGACAAAATACACCTTTATCTGTCATGGAATATCAGCCTGGAGGG	540	
Qy	547	GACTTGCTGTCACCTTTTGAATAGATATGAGGACCAAGTTAGATGAAAACCTGTACAGTTT	606	
Db	541	GACTTGCTGTCACCTTTTGAATAGATATGAGGACCAAGTTAGATGAAAACCTGTACAGTTT	600	
Qy	607	TACCTAGCTAGCTGATTTTGGCTGTTTCAAGCGTTTCACTGATGGGAATACGTGCATCGA	666	
Db	601	TACCTAGCTAGCTGATTTTGGCTGTTTCAAGCGTTTCACTGATGGGAATACGTGCATCGA	660	
Qy	667	GACATCAGCCTCAGAACATTTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT	726	
Db	661	GACATCAGCCTCAGAACATTTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT	720	
Qy	727	GGATCTGCCCGGAAAATGAATTCAAAACAGATGGTGAATGCCAAATCTCCCGATTGGGACC	786	
Db	721	GGATCTGCCCGGAAAATGAATTCAAAACAGATGGTGAATGCCAAATCTCCCGATTGGGACC	780	
Qy	787	CCAGATTACATGCTCCTGAAAGTGCTGACTGTGATGAAACGGGGATGAAAAGGCACCTAC	846	
Db	781	CCAGATTACATGCTCCTGAAAGTGCTGACTGTGATGAAACGGGGATGAAAAGGCACCTAC	840	
Qy	847	GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCCTATCAGATGATTTTATGGAGA	906	





Db 1201 CCGTCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTCGCGTTTGTGGGGTTTCG 1260  
QY 1267 TACAGCAAGGCACTGGGGATTCTTGGTGTAGATCTGAGTCTGTGTGTGCGGCTCTGGACTCC 1326  
Db 1261 TACAGCAAGGCACTGGGGATTCTTGGTGTAGATCTGAGTCTGTGTGTGCGGCTCTGGACTCC 1320  
QY 1327 CTTGCCAAGACTAGCTCCATCGAAAGAAAATCTTCTCATCAAAAGCAAGAGCTTACAAGAC 1386  
Db 1321 CTTGCCAAGACTAGCTCCATCGAAAGAAAATCTTCTCATCAAAAGCAAGAGCTTACAAGAC 1380  
QY 1387 TCTCAGCAAGTGTACAAGGT 1409  
Db 1381 TCTCAGCAAGTGTACAAGAT 1403

## RESULT 5

US-09-774-528-419  
; Sequence 419, Application US/09774528  
; Patent No. 6743619  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Dmanac, Radoje T.  
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 802  
; CURRENT APPLICATION NUMBER: US/09/774,528  
; CURRENT FILING DATE: 2001-01-30  
; NUMBER OF SEQ ID NOS: 441  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 419  
; LENGTH: 2162  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (364)..(2010)  
US-09-774-528-419

Query Match 63.6%; Score 963.2; DB 4; Length 2162;  
Best Local Similarity 99.7%; Pred. No. 1.1e-311;  
Matches 965; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGAGATGTTGAAGTTCAATATGGAGCGCGGAATCCTTTGGATGCTGTGCTGTGAA 60  
Db 358 GGGGAGATGTTGAAGTTCAATATGGAGCGCGGAATCCTTTGGATGCTGTGCTGTGAA 417  
QY 61 CCCATTGCCAACCGGCTCCAGCTGAATCTGTTCTTCAGGGGAAACACCCCTTTATG 120  
Db 418 CCCATTGCCAACCGGCTCCAGCTGAATCTGTTCTTCAGGGGAAACACCCCTTTATG 477  
QY 121 ACTCAACAGCAGATGCTCTCTTCCGAGAGGGATATTAGATGCCCTTTGTTCTC 180  
Db 478 ACTCAACAGCAGATGCTCTCTTCCGAGAGGGATATTAGATGCCCTTTGTTCTC 537  
QY 181 TTGAAGAAATGCAGTCAAGCTGCTCTCATGAAGATTAAAGCAGCTGAGCAACTTTGTCGG 240  
Db 538 TTGAAGAAATGCAGTCAAGCTGCTCTCATGAAGATTAAAGCAGCTGAGCAACTTTGTCGG 597  
QY 241 AAGTATTCGACACCACTAGCTGAGTTACAGAGCTCCAGGCTTCGGCAAGAGCACTTCGAA 300

Db 598 AAGTATTCGACACCACTAGCTGAGTTACAGAGCTCCAGCTTCGCAAGAGCACTTCGAA 657  
QY 301 GTCAAGAGTCTTCTAGCTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTGAAGAGAAAGCA 360  
Db 658 GTCAAGAGTCTTCTAGCTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTGAAGAGAAAGCA 717  
QY 361 ACCGGGACATCTATCTATGAAGTGAAGAGAGGCTTTATTTGGCCCGAGGAGCAG 420  
Db 718 ACCGGGACATCTATCTATGAAGTGAAGAGAGGCTTTATTTGGCCCGAGGAGCAG 777  
QY 421 GTTTCATTTTTTGAGGAAGCGGACATATTATCTCGAGCACAAGCCGCTGGATCCCC 480  
Db 778 GTTTCATTTTTTGAGGAAGCGGACATATTATCTCGAGCACAAGCCGCTGGATCCCC 837  
QY 481 CAATTACAGTATGCTTTTTCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCCT 540  
Db 838 CAATTACAGTATGCTTTTTCAGGACAAAATCACCTTTATCTGCTCATGGAATATCAGCCT 897  
QY 541 GGAGGGAGCTTGTCTGTCACCTTTTGAATAGATATGAGGACCAAGTTAGTGAATAAACCCTGATA 600  
Db 898 GGAGGGAGCTTGTCTGTCACCTTTTGAATAGATATGAGGACCAAGTTAGTGAATAAACCCTGATA 957  
QY 601 CAGTTTTTACCTAGCTGAGCTGATTTTGGCTGTTTTCAGAGCTTCATCTGATGGGATACGTG 660  
Db 958 CAGTTTTTACCTAGCTGAGCTGATTTTGGCTGTTTTCAGAGCTTCATCTGATGGGATACGTG 1017  
QY 661 CATCGAGACATCAAGCTCGAGAACTTCTGCTTTCAGCGCAGGACACACATCAAGCTGGTG 720  
Db 1018 CATCGAGACATCAAGCTCGAGAACTTCTGCTTTCAGCGCAGGACACACATCAAGCTGGTG 1077  
QY 721 GATTTTGGATCTGCCCGGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780  
Db 1078 GATTTTGGATCTGCCCGGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 1137  
QY 781 GGGACCCAGATTACATGCTCCTGAAGTCTGACTGTGATGAACCGGGATGGAAGGC 840  
Db 1138 GGGACCCAGATTACATGCTCCTGAAGTCTGACTGTGATGAACCGGGATGGAAGGC 1197  
QY 841 ACCTACGGCTGAGCTGTGACTGCTGCTGAGTGGGCTGATTGCCCTATGAGATGATTAT 900  
Db 1198 ACCTACGGCTGAGCTGTGACTGCTGCTGAGTGGGCTGATTGCCCTATGAGATGATTAT 1257  
QY 901 GGGAGATCCCTTTCGAGAGGAACTCTGCGAGAACTCTGCGAGAACTTCAATTAACATTATGAATTC 960  
Db 1258 GGGAGATCCCTTTCGAGAGGAACTCTGCGAGAACTTCAATTAACATTATGAATTC 1317  
QY 961 CAGCGGTT 968  
Db 1318 CAGGTTT 1325

## RESULT 6

US-09-916-204-1  
; Sequence 1, Application US/09916204  
; Patent No. 6638745  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164CIP  
; CURRENT APPLICATION NUMBER: US/09/916,204  
; CURRENT FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1133  
; TYPE: DNA  
; ORGANISM: Human  
US-09-916-204-1  
Query Match 50.2%; Score 760.8; DB 4; Length 1133;  
Best Local Similarity 99.7%; Pred. No. 5.3e-244;

Matches 762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGTGAA 60  
Db 48 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGTGAA 107  
Qy 61 CCCATTGCCAACCGGCGCTCCAGCTGAATCTGTTCTTCAGGGGAAACCACTTTATG 120  
Db 108 CCCATTGCCAACCGGCGCTCCAGCTGAATCTGTTCTTCAGGGGAAACCACTTTATG 167  
Qy 121 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 180  
Db 168 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 227  
Qy 181 TTTGAAGATGCACTAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 240  
Db 228 TTTGAAGATGCACTAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 287  
Qy 241 AAGTATTCGGACACCATAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 300  
Db 288 AAGTATTCGGACACCATAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 347  
Qy 301 GTCAAGAGTCTTTGAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA 360  
Db 348 GTCAAGAGTCTTTGAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA 407  
Qy 361 ACCGGGACATCTATGCTATGAAGTGCAGGTGGTAAGAGAGAAAGCA 420  
Db 408 ACCGGGACATCTATGCTATGAAGTGCAGGTGGTAAGAGAGAAAGCA 467  
Qy 421 GTTTTCATTTTTCAGGAGAGCGGAAACATATTATCTCGAAGCAACAGCCGTTGATCCCC 480  
Db 468 GTTTTCATTTTTCAGGAGAGCGGAAACATATTATCTCGAAGCAACAGCCGTTGATCCCC 527  
Qy 481 CAATTACAGTATGCTTTTCAGGACAAATAATCCTTTATCTGCTGATGATATCAGCCT 540  
Db 528 CAATTACAGTATGCTTTTCAGGACAAATAATCCTTTATCTGCTGATGATATCAGCCT 587  
Qy 541 GGAGGGACCTGCTGCTCACTTTTGAATAGATATGAGACCACTTTAGATGAAACCTGATA 600  
Db 588 GGAGGGACCTGCTGCTCACTTTTGAATAGATATGAGACCACTTTAGATGAAACCTGATA 647  
Qy 601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTTTCACAGCGTTCACTGATGGGATACGTG 660  
Db 648 CAGTTTTACCTAGCTGAGCTGATTTTGGCTTTCACAGCGTTCACTGATGGGATACGTG 707  
Qy 661 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACATCAAGCTGGTG 720  
Db 708 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACATCAAGCTGGTG 767  
Qy 721 GATTTTGGATCTGCCGGAATGAATTCAAACAGATGTTGAA 764  
Db 768 GATTTTGGATCTGCCGGAATGAATTCAAACAGATGTTGAA 811

## RESULT 7

US-10-282-048-1

; Sequence 1, Application US/10282048  
; Patent No. 6692948  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001164CIP-DIV  
; CURRENT APPLICATION NUMBER: US/10/282,048  
; CURRENT FILING DATE: 2002-10-29  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1133  
; TYPE: DNA  
; ORGANISM: Human

US-10-282-048-1

Query Match 50.2%; Score 760.8; DB 4; Length 1133;  
Best Local Similarity 99.7%; Pred. No. 5.3e-244;  
Matches 762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGTGAA 60  
Db 48 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGTGAA 107  
Qy 61 CCCATTGCCAACCGGCGCTCCAGCTGAATCTGTTCTTCAGGGGAAACCACTTTATG 120  
Db 108 CCCATTGCCAACCGGCGCTCCAGCTGAATCTGTTCTTCAGGGGAAACCACTTTATG 167  
Qy 121 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 180  
Db 168 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 227  
Qy 181 TTTGAAGATGCACTAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 240  
Db 228 TTTGAAGATGCACTAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 287  
Qy 241 AAGTATTCGGACACCATAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 300  
Db 288 AAGTATTCGGACACCATAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 347  
Qy 301 GTCAAGAGTCTTTGAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA 360  
Db 348 GTCAAGAGTCTTTGAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA 407  
Qy 361 ACCGGGACATCTATGCTATGAAGTGCAGGTGGTAAGAGAGAAAGCA 420  
Db 408 ACCGGGACATCTATGCTATGAAGTGCAGGTGGTAAGAGAGAAAGCA 467  
Qy 421 GTTTTCATTTTTCAGGAGAGCGGAAACATATTATCTCGAAGCAACAGCCGTTGATCCCC 480  
Db 468 GTTTTCATTTTTCAGGAGAGCGGAAACATATTATCTCGAAGCAACAGCCGTTGATCCCC 527  
Qy 481 CAATTACAGTATGCTTTTCAGGACAAATAATCCTTTATCTGCTGATGATATCAGCCT 540  
Db 528 CAATTACAGTATGCTTTTCAGGACAAATAATCCTTTATCTGCTGATGATATCAGCCT 587  
Qy 541 GGAGGGACCTGCTGCTCACTTTTGAATAGATATGAGACCACTTTAGATGAAACCTGATA 600  
Db 588 GGAGGGACCTGCTGCTCACTTTTGAATAGATATGAGACCACTTTAGATGAAACCTGATA 647  
Qy 601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTTTCACAGCGTTCACTGATGGGATACGTG 660  
Db 648 CAGTTTTACCTAGCTGAGCTGATTTTGGCTTTCACAGCGTTCACTGATGGGATACGTG 707  
Qy 661 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACATCAAGCTGGTG 720  
Db 708 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACATCAAGCTGGTG 767  
Qy 721 GATTTTGGATCTGCCGGAATGAATTCAAACAGATGTTGAA 764  
Db 768 GATTTTGGATCTGCCGGAATGAATTCAAACAGATGTTGAA 811

## RESULT 8

US-09-949-016-2640

; Sequence 2640, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768



; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2726 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-422-699A-12

Query Match 14.9%; Score 225.6; DB 2; Length 2726;

Best Local Similarity 54.0%; Pred. No. 3.3e-64; Indels 15; Gaps 3;

Matches 534; Conservative 0; Mismatches 439; Indels 15; Gaps 3;

QY 200 CTGCTCTGATGAAGATTAAACACGCTGAGCAACTTTGTCGCGAAGTATTCCGACACCATAG 259

DB 243 CCGAATCTGGCCGAGCAAGTACGTGCGCACTTCTTGAGTGGCGGAGCCCATCGTGG 302

QY 260 CTGAGTTACAGAGCTCCAGCTTTCGCGAAAGGACTTCGAAAGTCAGAAAGTCTTTGAGTT 319

DB 303 TGAGGCTTAAGGAGTCCGACTGCAGAGGACGACTTCGAGATTCTGAAGTGTATCGGAC 362

QY 320 GTGCTCACTTTGTAAGTGCAGGTGTAGAGAGAAAGCAACGCGGACATCTATGCTA 379

DB 363 CGCGGCGTTTCAGCGAGTACGCGTAGTGAAGATGAAGACAGCGGCGGAGTGTGCGCA 422

QY 380 TGAAGTGAAGAAAGAGCTTTATTGCGCCAGGAGGAGTTTCAATTTTGGAGAG 439

DB 423 TGAAGATCATGAAGTGGACATGCTGAAGGGGCGAGGTGCTGTCTTCGGTGAGG 482

QY 440 AGCGGAACATATTATCTCGAAGCACAAAGCCGCTGGATCCCGCAATTAAGTATGCTTTTC 499

DB 483 AGAGGAGCGTTTGGTGAATGGGACCGCGGTGGATCAACGAGCTGCACTTCGCGCTTC 542

QY 500 AGGACAAATACCTTTATCTGCTCATGAAATATCAGCTTGCAGGGGAGCTTCTGTCTAC 559

DB 543 AGGATGAAGTAACTACCTGTCTGCTCATGAGTATTAAGTGGGCGGAGCTGCTGACAC 602

QY 560 TTTTGAATAGATGAGACACGAGTATGATAAAACCTGATACAGTTTCTACTAGCTGAGC 619

DB 603 TGCTGACCAAGTTTGGGAGCGGATTCGCGCGAGATGGCGCGCTTCTACTTGGCGAGA 662

QY 620 TGATTTTGGCTGTTTCAAGCGTTTCACTGATGGGATACGTGCAATCGAGATCAAGCGCTG 679

DB 663 TTGTCATGGCCATAGACTCGGTGACCGCGTGGCTAGCTGACAGGGAGCATCAACCCG 722

QY 680 AGAATCTCTGTTGACCGCACAGGACATCAAGCTGTTGATTTTGGATCTGCGCGA 739

DB 723 ACAACATCTGCTGGAGCGCTGTGGCCACATCGCGCTTGGCGAGCTTCGGCTCTTGCCTCA 782

QY 740 AATGAATTCACAAAGATGGTGAATGCAAACTCCCGATTGGGACCCAGATTACATGG 799

DB 783 AGCTGGCGGAGATGGAAACGGTGGCTGCTGCTGCTGGGACCCAGACTACCTGT 842

QY 800 CTCTGAGTGTCTGA---CTGTGATGAACGGGATGAAAGGACCTTACGGCTGAGCT 856

DB 843 CCCCAGAGATCTTCAGGCTGTGGCGGTGGGCTGGGACAGGAGCTACGGGCGCGAGT 902

QY 857 GTGACTGGTGTGCTGAGTGGGCTGATGGCTATGAGATGATTTATGGAGATCCCGCTTCG 916

DB 903 GTGACTGGTGGCGCTGGGTGTATTTCGCTTATGAATGTTCTATGGGACAGCGCTTCT 962

QY 917 CAGAGGGAACCTTCGCGAGAACCTTCAATAATTAATTTCCAGCGGTTTTTGAAT 976

DB 963 ACGGGATTCACGGCGGAGACCTATGGCAAGATCGTCCACTACAAGGAGACCTCTCTC 1022

QY 977 TTCCAGATGACCCCAAGATGAGCAGT---GACTTTCTTGATCTGATTAAGTCAAGCTTGTTGT 1033

DB 1023 TGCCGCTGTGTGACCAAGGGGTCCCTGAGGAGGCTCGAGACTTCAATTCAGCGGTTGCTGT 1082

QY 1034 CGCGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTTGTGC-----CATCCTTTCT 1084

DB 1083 GTCCCCCGGAGACAGCGCTGGCGGGGTGGAGCAGGCGATTCGCGACATCCCTTCT 1142

QY 1085 TCTCTAAATTTGACTGGAAACAACATTCGTAACTCTCTCTCCCCCTTCGTTCCCAACCTCA 1144

DB 1143 TCTTTGGCTCGACTGGGATGGTCTCCGGGACAGCGTGGCCCCCTTTACACCGGATTCG 1202

QY 1145 AGTCCACGATGACACCTCCAAATTTGA 1172

DB 1203 AAGTGCCACCGACACATGCAACTCGA 1230

RESULT 10

US-08-422-706B-12

; Sequence 12, Application US/08422706B

; Patent No. 5977333

; GENERAL INFORMATION:

; APPLICANT: Brook, J. David

; APPLICANT: Housman, David E.

; APPLICANT: Shaw, Duncan J.

; APPLICANT: Harley, Helen G.

; APPLICANT: Johnson, Keith J.

; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC

; TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith &amp; Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02713

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/422,706B

; FILING DATE: 14-APR-1995

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/284,543

; FILING DATE: 08-AUG-1994

; APPLICATION DATA:

; APPLICATION NUMBER: US 08/023,612

; FILING DATE: 26-FEB-1993

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/839,255

; FILING DATE: 20-FEB-1992

; APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/01545

; FILING DATE: 19-FEB-1993

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB93/00253

; FILING DATE: 05-FEB-1993

; APPLICATION DATA:

; APPLICATION NUMBER: GB9202485.0

; FILING DATE: 06-FEB-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: MIT-5830A2

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2726 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-422-706B-12

Query Match 14.9%; Score 225.6; DB 2; Length 2726;

Best Local Similarity 54.0%; Pred. No. 3.3e-64; Indels 15; Gaps 3;

Matches 534; Conservative 0; Mismatches 439; Indels 15; Gaps 3;

200 CTGCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTTGTCCGAAAGTATTCGACACCATAG 259  
243 CCGAACCTGGCCAGGACAAGTACGTGGCCGACTTCTTGCAGTGGCGGAGCCCATCGTGG 302  
260 CTGAGTTACAGGAGCTCCAGCCTTCGCGAAAGACTTCGAAGTCAAGAGTCTTGTAGTT 319  
303 TGAGGCTTAAGAGGTCGAGTCCGAGTCCGAGGAGCAGCTTCGAGATTCGAAAGTATCGGAC 362  
320 GTGCTCACTTTGCTGAAGTGCAGTGTGAAGAGAAAGCAACCGGGGACATCTATGCTA 379  
363 GCGGGGCTTCAGGAGGTAGCGTAGTGAAGTGAAGCAGACGCGCAGGTGTATGCCA 422  
380 TGAAGTGAATGAAGAAAGGCTTTATTTGCCCCAGGAGCAGGTTTCAATTTTTTGAAGAG 439  
423 TGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGCGAGGTGCTGCTCCGTGAGG 482  
440 AGCGGAACATATTATCTCGAAGACAAAGCCCGTGGATCCCCCAATTAAGTATGCTCTTC 499  
483 AGAGGACGCTGTTGGTGAATGGGACCGCGGCTGGATCAAGCAGCTGCACTTCGCTTCC 542  
500 AGACAAAATACCTTTATCTGTCATGAATATACAGCTGAGGGGAGCTGCTGTCAC 559  
543 AGATGAAGTACTACTGCTGCTGTCATGAGTATTAAGTGGCGGGGAGCTGCTGACAC 602  
560 TTTTGAATAGATATGAGGACCAAGTTAGATGAAGAACCTGTATACAGTTTACCTAGCTGAGC 619  
603 TGCTGACCAAGTTTGGGAGCGGATTCGCGCCGAGATGGCGCTTCTACTGCGGAGA 662  
620 TGATTTTGGCTGTTACAGAGCTTCATCTGATGGGATGAGTGCATCGAGACATCAAGCTG 679  
663 TTGCTATGGCCATAGACTCGGTGACCGGCTTGGCTACGTGTCACAGGAGATCAAAACCCG 722  
680 AGAATCTTCGTTGACCGCACAGGACACATCAAGCTGTGGATTTTGGATCTGCCGGA 739  
723 ACAATCTCTGCTGAGACCGTGTGGCCACATCCGCTTGGCGGACTTTCGGCTCTTGGCTCA 782  
740 AATGAATTCACAAAGATGTTGAATGCCAAATCCCGATTGGGACCCAGATTACATGG 799  
783 AGCTGGCGGAGATGGAACGCTGGCTGCTGGTGGCTGCGGACCCAGACTACTGT 842  
800 CTCTGAAGTCTGA----CTGTGATGAACCGGGATGAAAGGACCTACGGCTGGACT 856  
843 CCCCCGAGATCTCTGAGCTGTGGCGGCTGGGCTGGGACAGGACAGCTACGGGCGGAGT 902  
857 GTGACTGCTGCTGAGTGGCGGTGATTCCTATGAGATGATTTATGGAGATCCCGCTTCG 916  
903 GTGACTGTTGGCGCTGGGTGATTCGCCCTATGAATGTTCTATGGGACAGACGCGCTTCT 962  
917 CAGAGGAACTCTCTGCAGAACCTTCAATAACATTTATGAATTTCCAGCGGTTTTTGAAT 976  
963 ACGCGATTCACGGCGGAGACCTATGGCAAGATCGTCCACTACAGGAGCACCTCTCTC 1022  
977 TTCAGATGATCCCAAGTGAAGT---GACTTTCTGATCTGATTCGAATCAAGTGTGTT 1033  
1023 TGCGCTGTGGTGAAGGAGGCTCCCTGAGGAGGCTCGAGACTTCATTCAGCGGTGCTGT 1082  
1034 GCGGCCAAGAGAGAGACTGAAGTTGAAGTCTTTGCTGC-----CATCTTTCT 1084  
1083 GTCCCCCGGAGACACGCTGCGCGGGGTGGAGCGAGCTTCCCGACACATCCCTTCT 1142  
1085 TCTCTAAATTTGACTGGAAACAAATTCGTAACTCTCTCCCCCTTCTGTTCCACCTCA 1144  
1143 TCTTTGCGCTCGACTGGATGCTCTCGGACAGCGGTGCCCCCTTTACACCGGATTCG 1202  
1145 AGTCCGACGATGACACCTCCAATTTGA 1172  
1203 AAGTGTCCACCGACACATGCAACTTGA 1230

RESULT 11

US-08-422-699A-8

; Sequence 8, Application US/08422699A

Patent No. 5955265  
GENERAL INFORMATION:  
APPLICANT: Brook, J. David  
APPLICANT: Housman, David E.  
APPLICANT: Shaw, Duncan J.  
APPLICANT: Harley, Helen G.  
APPLICANT: Johnson, Keith J.  
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC  
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02713  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,699A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/422,706  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/023,612  
FILING DATE: 26-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/839,255  
FILING DATE: 20-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/01545  
FILING DATE: 19-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00253  
FILING DATE: 05-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB9202485.0  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-5830A2  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2511 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1746  
US-08-422-699A-8

Query Match 14.4%; Score 218.8; DB 2; Length 2511;  
Best Local Similarity 54.5%; Pred. No. 6e-62;  
Matches 511; Conservative 0; Mismatches 412; Indels 15; Gaps 3;  
QY 250 GACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCGAAAGACTTCGAAGTCAAGT 309  
DB 43 GCCATCGTGTGAGGCTTAAGGAGTCCGACTCGAGGGGACGACTTCGAGATTCGAG 102  
QY 310 CTTGTAGGTTGTGTCACCTTTGCTGAAGTGCAGGTGTTGCTGAAGTGAAGAAAGCAACCGGGAC 369

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Db 103 GTGATCGGACGCGGGCGTTTCAGCGAGTAGTGAAGATGAAGACAGCGGCCAG 162
Qy 370 ATCTATGCTATGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 429
Db 163 GTGATGCTATGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 222
Qy 430 TTTGAGGAGAGCGGAGATATATCTCGAAGCACAAGCCGCTGATCCCGCAATACAG 489
Db 223 TTCCGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 282
Qy 490 TATCCCTTTCCAGGACAAAATACCTTTATCTGCTATGGAATATCAGCCCTGGAGGGAG 549
Db 283 TTCCGCTTCCAGGATGAGAACTACCTGTACCTGCTCATGGTATTAAGTGGCGGGAG 342
Qy 550 TTGCTGTACATTTTGAATAGATATGAGACAGATGATGAATAAACCCTGATACAGTTTAC 609
Db 343 CTGCTGACACTGCTGAGCAAGTTTGGGAGCGGATTCGCGCGAGATGGCGGCTTCTAC 402
Qy 610 CTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTCATCTGATGGATACGTCGATCGAGAC 669
Db 403 CTGGCGGAGATGTCATGGCCCATAGATCTGGTGCCCGCTTGGCTACGTCAGAGGAC 462
Qy 670 ATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGA 729
Db 463 ATCAACCCGACAACTCTGCTGACCGCTGTGGCCACATCGCCCTGGCGGACTTCGGC 522
Qy 730 TCTCCCGGAAATGAATTAACAAGATGGTGAATGCCAACTCCCGATGGGACCCCA 789
Db 523 TCTTGGCTCAAGCTGCGGGCAGATGGAACGGTGGCGGTGCTGGTGGCTGGGACCCCA 582
Qy 790 GATTACATGGCTCTGTA---AGTCTGACTGTGATGAACGGGATGAAAAGGCACTAC 846
Db 583 GACTACCTGTCCCGGAGATCTGAGGCTGTGGCGGTGGGCTGGGACAGGAGTAC 642
Qy 847 GGCCTGAGCTGTGACTGTGCTGAGTGGCGGTGATTCCTATGAGATGATTTATGGGAGA 906
Db 643 GGGCCGAGTGTGACTGTGGCGCTGGGTGATTTCCGCTATGAATGTTCTATGGGCG 702
Qy 907 TCCCGCTTCCGAGGAGAACTCTGCCAGAACCTTCAATCAACATGATTAATTTCCAGCG 966
Db 703 ACGCCCTTCTACGCGGATTCACGCGGAGACCTATGCGCAAGATCGTCCACTACAGGAG 762
Qy 967 TTTTGAATTTCCAGATGACCCCAAGTGAAGAGT---GACTTTCTTGTATCTGATTCAA 1023
Db 763 CACTCTCTCTGCGCTGTGGAGAGAGGGTCCCTGAGGAGGCTCGAGACTTCATTCAG 822
Qy 1024 AGCTTGTGTGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1074
Db 823 CGGTTGTGTGTCCTCCCGGAGACACGCTGGCGGGGTGGAGCAGCGGACTTCGCGACA 882
Qy 1075 CATCTTTCTTCTCTAAATTTGACTGGGACAAACATTCGTAACCTCTCTCCCGCTTCGTT 1134
Db 883 CATCCCTTCTTCTTGTGGCTGAGCTGGGATGGTCTCCGCGGACAGCGTGCCTTTCATA 942
Qy 1135 CCCACCTCAAGTCCGACGATGACACCTTCCAAATTTGA 1172
Db 943 CCGGATTTGAGAGTGCACCGACACATGCACTTCCA 980

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RESULT 12
US-08-422-706B-8
; Sequence 8, Application US/08422706B
; Patent No. 5977333
; GENERAL INFORMATION:
; APPLICANT: Brook, J. David
; APPLICANT: Housman, David E.
; APPLICANT: Shaw, Duncan J.
; APPLICANT: Harley, Helen G.
; APPLICANT: Johnson, Keith J.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
; DYSTROPHY GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,706B
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,543
; FILING DATE: 08-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,612
; FILING DATE: 26-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/839,255
; FILING DATE: 20-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01545
; FILING DATE: 19-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00253
; FILING DATE: 05-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB9202485.0
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5830A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2511 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1746
; US-08-422-706B-8

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Query Match 14.4%; Score 218.8; DB 2; Length 2511;
Best Local Similarity 54.5%; Pred. No. 6e-62;
Matches 511; Conservative 0; Mismatches 412; Indels 15; Gaps 3;

Qy 250 GACACCATAGCTGAGTTACAGGAGCTCCAGCCCTTCGSCAAAGGACTTCGAAGTCAGAAGT 309
Db 43 GCCATCGTGTGAGGCTTAAAGAGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 102
Qy 310 CTTGTAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTGAAGAGAGAAAGCAACCCGGGAC 369
Db 103 GTGATCGGACGCGGGCGTTTCAGCGAGGTAGCGGTAGTGAAGATGAAGCAGACGCGGCCAG 162
Qy 370 ATCTATGCTATGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 429
Db 163 GTGTATGCCATGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGCGGAGGTGTCGTGC 222
Qy 430 TTTGAGGAGAGCGGAGCAATATTTATCTCGAAGCACAAGCCGCTGGATCCCGCAATACAG 489
Db 223 TTCCGTGAGGAGAGGAGCGGTGTTGGTGAATGGGAGCGGCGGTGGATCAGCGAGTGCAC 282
Qy 490 TATGSCCTTTTCAGGACAAAATACCTTTTATCTGGTCAATGGAATATCAGCCTGGAGGGGAC 549

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283 TTGCTGCTCCAGGATGAGAACTACCTGTACCTGGTATGAGTATTACGTGGCGGGAC 342  
550 TTGCTGCTCACTTTTGAATAGATAGAGACAGTTAGTAAACCTGATACAGTTTAC 609  
343 CTGCTGACATGCTGACCAAGTTTGGGAGGGATTCGGCCGAGATGGCGCTTCTAC 402  
610 CTAGCTGAGCTGATTTTGGCTGTTTACAGCGCTTCATCTGATGGATAGCTGCGATCGAGAC 669  
403 CTGGCGGAGATTGTCTGCGCATAGACTCGGTGCACCGCTTGGCTAGCTGCGACAGGAC 462  
670 ATCAAGCTGAGAACATTCGTTGACCGCAGGACACATCAAGCTGGTGGATTTGGA 729  
463 ATCAAAACCGACAACTCTGCTGACCGCTGTGGCCACATCGCTCTGGCGGCTTGGC 522  
730 TCTGCGCGGAAATGAAATCAAAACAGATGCTGAATGCCAACTCCCGATTGGGACCCA 789  
523 TCTGCTCAAGCTGCGGCGAGATGGAACGGTGGCGCTGCTGGTGGCTGGGACCCCA 582  
790 GATTACATGGCTCCTGA---AGTGTGACTGTGATGAACGGGATGGAAGGACACCTAC 846  
583 GACTACCTGTCCTCCGAGATCCTGCAGGCTGTGGCGGTGGCTGGGACAGGAGCTAC 642  
847 GGCTGACTGTGACTGGTGGTGTAGTGGCGTGAATTCCTATGAGATGATTATGGGAGA 906  
643 GGGCCGAGTGTGACTGGTGGCGCTGGTGTATTCGCTTATGAAATGTTCTATGGGAG 702  
907 TCCCTCTTCGAGGGAACCTCTGCCAGAACCTTCAATTAACATTAATGATTTCCAGCG 966  
703 ACGCCCTTTCACGCGGATTCCAGCGGAGACCTATGGCAAGATCGCTCACTACAAGGAG 762  
967 TTTTGAATTTCCAGATGACCCCAAGTGTGAGCT---GACTTTCTTGATCTGATTCAA 1023  
763 CACTCTCTCTGCGGTGGAGAGGGTCCCTGAGAGGCTCGAGACTTCATTTCAG 822  
1024 AGCTGTTGTGGCGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCTC----- 1074  
823 CGGTGTGTGTGCTCCCGAGACACCGCTGGCGGGTGGAGCAGCGGCTTCCGAGCA 882  
1075 CATCTCTTCTCTCTAAATTTGACTGGAACACATTCGTAACCTCTCTCCCGCTTGGTT 1134  
883 CATCTCTTCTCTTGTGGCTGAGTGGATGGTCTCCGGGACAGCGTGGCCCCCTTACA 942  
1135 CCCACCTCAAGTCCGACGATGACACCTCCAAATTTGA 1172  
943 CCGGATTTCAAGTGGCCCGGACACATGCACTTCA 980

RESULT 13

US-08-484-044-11  
; Sequence 11, Application US/08484044  
; Patent No. 5552282  
; GENERAL INFORMATION:  
; APPLICANT: Caskey, C. T.  
; APPLICANT: Fu, Ying-Hui  
; APPLICANT: Friedman, David L.  
; APPLICANT: Pizzuti, Antonio  
; APPLICANT: Fenwick, Raymond G.  
; TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Fulbright & Jaworski, L.L.P.  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,044  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: US 08/019,940  
APPLICATION NUMBER: US 08/019,940  
FILING DATE: 19-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5443  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5325  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3182 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-484-044-11

Query Match 14.4%; Score 218.4; DB 1; Length 3182;  
Best Local Similarity 54.5%; Pred. No. 9.6e-62;  
Matches 510; Conservative 0; Mismatches 411; Indels 15; Gaps 3;

QY 252 CACCATAGCTGAGTTACAGGAGCTCCAGCTTCGGCAAGAGCTTCGAAGTCAGAACTCT 311  
DB 743 CATCGTGGTGAAGGCTTAAAGAGGCTCGAGCTGCAGAGGAGCAGCTTCGAGATTCTGAAGGT 802  
QY 312 TGTAAGTGTGGTCACTTTGCTCAAGTGCAGAGTGGTAAGAGAGAAAGCAACCGGGGACAT 371  
DB 803 GATCGAAGCGGGCGCTTCAGCAGGTAGCGGTAGTGAAGATGAAGCAGACGGCCAGGT 862  
QY 372 CTATGCTATGAAGTGAAGAAAGGCTTTATTTGGCCAGAGCAGGTTTCATTTTT 431  
DB 863 GTATGCCATGAAGATCATGAACAAAGTGGGACATGCTGAAGAGGGCGAGGTGCTGCTT 922  
QY 432 TGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCAAATACAGTA 491  
DB 923 CCGTGAAGAGAGGAGCGTGTGGTGAATGGGAGCCGGCGGTGATCACGAGCTGCACTT 982  
QY 492 TGCTTTTCAGGACAAAATCACCTTTATCTGGTCAATGGAATATCAGCTCGAGGGGACTT 551  
DB 983 CGCTTCCAGGATGAGAACTACCTGTACCTGGTCAATGGAGTATTAAGTGGCGGGGACCT 1042  
QY 552 GCTGTCACTTTTGAATAGATATGAGGACCAAGTTAGATGAAGAACTGATACAGTTTACCT 611  
DB 1043 GCTGACACTGCTGAGCAAGTTTGGGAGCGGATTCGGCCGAGATGGCGGCTTCTACCT 1102  
QY 612 AGCTGAGCTGATTTGGCTGTTTCAAGCGTTTATCTGATGGGATAGTGTGATCGAGACAT 671  
DB 1103 GCGGAGATTGTTCATGGCCATAGACTCGGTGACCGGCTTGGCTTGGCTGACAGGACAT 1162  
QY 672 CAAGCTGAGAACATTTCTGTTGACCGCAGCAGACACATCAAGCTGGTGAATTTGATC 731  
DB 1163 CAACCCGACACATCTGCTGAGCCGCTGTGGCCATATCCGCTTGGCCGCTTGGGCTC 1222  
QY 732 TGCCGCGAAATGAATTTCAAAAGATGTAATGCAAACTCCGATTTGGGACCCCGAGA 791  
DB 1223 TTGCTCAAGCTGCGGCGAGATGGAACGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1282  
QY 792 TTACATGGCTCCTGA---AGTGTGCTGATGATGAACGGGATGGAAGGACACCTACGG 848  
DB 1283 CTACCTGTCCCGGAGATCCTGAGGCTGTGGCGGTGGGCGCTGGGACAGGACAGTACGG 1342  
QY 849 CTTGAGCTGTGACTGTGTGTGCTGAGTGGCTGATTTGCTATGAGATGATTTATGGAGATC 908  
DB 1343 GCGGAGTGTGACTGTGTGGCGCTGGTGTATTGCTGCTATGAATGTTCTATGGGAGAC 1402  
QY 909 CCGCTTTCGAGAGGAGAACCTCTGCCAGAACCTTCAATAACATTTATGAATTTCCAGCGGTT 968

Db 1403 GCCCTTCTACGGATTCCACGGCGAGACCTATGGCAAGATCTCCACTACAAGGACCA 1462  
Qy 969 TTTGAAATTTCCAGATGACCCCAAGTGAGCAGT---GACTTTCTTGATCTGATCAAAAG 1025  
Db 1463 CCTCTCTCTGCGCTGGTGGACGAAGGGGTCCCTGAGGAGGCTCGAGACTTCATTACAGC 1522  
Qy 1026 CTTGTTGTCGGCCAGAAAGAGAGACTCAAGTTTGAAGGCTTTTGCTGC-----CA 1076  
Db 1523 GTTGCTGTGTCCTCCCGGAGACACCGCTGGGCGGGTGGAGCAGGCGACTTCGGGACACA 1582  
Qy 1077 TCCTTTCTTCTCTAAAATTTGACTGGAACAAACATTCGTAACCTCTCTCCCGCCCTTCGTTCC 1136  
Db 1583 TCCCTCTCTCTTGGCCTCGACTGGATGGTCTCCGGGACAGCGTGCCCCCTTTACACC 1642  
Qy 1137 CACCTCTAAGTCCGACGATGACACTCCATTTTGA 1172  
Db 1643 GGATTTGGAAGTCCACCGACACATCACTTCGA 1678

## RESULT 14

US-09-804-471A-3

; Sequence 3, Application US/09804471A

; Patent No. 6479269

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001164

; CURRENT APPLICATION NUMBER: US/09/804,471A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 174493

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(174493)

; OTHER INFORMATION: n = A,T,C or G

US-09-804-471A-3

Query Match 14.3%; Score 216.2; DB 4; Length 174493;  
Best Local Similarity 96.5%; Pred. No. 8.7e-60;  
Matches 221; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 1287 TCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCGCTGCCAAGACTAGTCCAT 1346  
Db 171282 TTTTCTCTACTAGGTCTGTGTGTCGGGTCTGGACTCCCGCTGCCAAGACTAGTCCAT 171341  
Qy 1347 GGAAGAGAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACAAGTGTCAAA 1406  
Db 171342 GGAAGAGAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACAAGTGTCAAA 171401  
Qy 1407 GGTATTTATTTCCGACGCGGCTCTCTTCTTGTCTCAGGATCTCCCGTCCGTATATGC 1466  
Db 171402 GGTATTTATTTCCGACGCGGCTCTCTTCTTGTCTCAGGATCTCCCGTCCGTATATGC 171461  
Qy 1467 CAAGGGATCCGCGCGGCGCTGCTGCTGCTGAGCGCGCTGATCCGTA 1515  
Db 171462 CAAGGGATCCGCGCGGCGCTGCTGCTGCTGAGCGCGCTGATCCGTA 171510

## RESULT 15

US-10-238-709-3

; Sequence 3, Application US/10238709

; Patent No. 6680188

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; CURRENT FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 174493  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(174493)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-238-709-3

Query Match 14.3%; Score 216.2; DB 4; Length 174493;  
Best Local Similarity 96.5%; Pred. No. 8.7e-60;  
Matches 221; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 1287 TCTTGGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCGCTGCCAAGACTAGTCCAT 1346  
Db 171282 TTTTCTCTACTAGGTCTGTGTGTCGGGTCTGGACTCCCGCTGCCAAGACTAGTCCAT 171341  
Qy 1347 GGAAGAGAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACAAGTGTCAAA 1406  
Db 171342 GGAAGAGAACTTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACAAGTGTCAAA 171401  
Qy 1407 GGTATTTATTTCCGACGCGGCTCTCTTCTTGTCTCAGGATCTCCCGTCCGTATATGC 1466  
Db 171402 GGTATTTATTTCCGACGCGGCTCTCTTCTTGTCTCAGGATCTCCCGTCCGTATATGC 171461  
Qy 1467 CAAGGGATCCGCGCGGCGCTGCTGCTGCTGAGCGCGCTGATCCGTA 1515  
Db 171462 CAAGGGATCCGCGCGGCGCTGCTGCTGCTGAGCGCGCTGATCCGTA 171510

Search completed: March 19, 2005, 14:35:00

Job time : 271.502 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 07:45:41 ; Search time 4592.53 Seconds  
(without alignments)  
12556.766 Million cell updates/sec

Title: US-10-724-594-1  
Perfect score: 1515  
Sequence: 1.gggagatgtgaattcaa.....tctgagcgcgtatccgta 1515

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	602.6	39.8	698	5	BP146990	BP146990
2	521.2	34.4	1085	5	BM904785	BM904785 AGENCOURT
3	478	31.6	492	7	CR746615	CR746615
4	452.8	29.9	600	4	EG808196	EG808196 2082-86 M
5	425.4	28.1	485	7	CR746792	CR746792 CR746792
6	423.8	28.0	427	4	BG944539	BG944539 ax51f11.x
7	413.2	27.3	617	5	BQ417810	BQ417810 ik51b06.y
8	380	25.1	481	7	CN682405	CN682405 E0164B04-
9	378	25.0	479	7	CN678533	CN678533 E0112C12-
10	351.4	23.2	490	2	BF562826	BF562826 UI-R-BJ0p
11	344.2	22.7	821	4	B1654262	B1654262 603280370
12	329.2	21.7	450	9	CG501400	CG501400 OST45250
13	328.8	21.7	423	2	BF344814	BF344814 602014091
14	327	21.6	449	9	CG501399	CG501399 OST45249
15	318.2	21.0	512	9	CG652891	CG652891 OST417039
16	314.2	20.7	340	2	BF380737	BF380737 IL2-UT007
17	312.6	20.6	582	5	BX516291	BX516291 BX516291
18	281.6	18.6	521	1	AI882189	AI882189 ul31e08.y
19	281.4	18.6	355	8	CC325092	CC325092 XL068 Bay
20	278.8	18.4	539	2	AW525215	AW525215 UI-R-BJ0p
21	276.4	18.2	325	3	EC008127	EC008127 Homo sapi
22	272.6	18.0	336	9	CG869028	CG869028 AB0155 Sa
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24	262.4	17.3	335	2	BF763211	BF763211 IL2-CS004

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	26	251.8	16.6	423	2	BB827314
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	29	246.2	16.3	289	4	BF944809
	30	246	16.2	508	6	CB783081
	31	245.8	16.2	547	7	CF744826
	32	245.8	16.2	647	7	CF744580
	33	244.8	16.2	801	5	BU475240
	34	244.8	16.2	847	5	BU467302
	35	243.4	16.1	807	7	CK147448
	36	240.8	15.9	401	6	BY602044
	37	238.8	15.8	2688	3	BC024150
	38	237.2	15.7	2862	3	BC056615
	39	236	15.6	1478	9	AY408842
	40	233.6	15.4	605	5	BP168081
	41	233.4	15.4	563	6	CD310916
	42	231.6	15.3	370	5	BY021399
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	44	225.2	14.9	1600	3	BC038993
	45	222	14.7	400	1	AL360718

## ALIGNMENTS

RESULT 1  
BP146990

LOCUS  
DEFINITION

ACCESSION  
BP146990

VERSION  
BP146990.1

KEYWORDS  
EST.

SOURCE  
Sus scrofa (pig)

ORGANISM  
Sus scrofa

REFERENCE  
1 (bases 1 to 698)

AUTHORS  
Uenishi H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamasima, N. and Awata, T.

TITLE  
PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries

JOURNAL  
Nucleic Acids Res. 32 (1), D484-D488 (2004)

COMMENT  
Contact: Hirohide Uenishi  
Animal Genome Laboratory, Genome Research Department  
National Institute of Agrobiological Sciences  
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
Tel: +81-29-838-8627  
Fax: +81-29-838-8627  
Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in  
Animal Genome Research Program (Japan) by National Institute of  
Agrobiological Sciences and STAFF-Institute

Single pass sequencing of clones derived from oligo-capped cDNA  
library

Vector sequences were eliminated by RepeatMasker version 2002/07/13  
and crossmatch version 0.990319

Low quality bases were trimmed based on the quality values.

FEATURES  
source

Location/Qualifiers  
1..698

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9823"

/clone="OVRM10025B09"

/tissue\_type="ovary"

/dev\_stage="adult"

/clone\_lib="full-length enriched swine cDNA library, adult  
ovary"

ORIGIN

Query Match 39.8%; Score 602.6; DB 5; Length 698;  
Best Local Similarity 91.4%; Pred. No. 2.9e-172;

BP146990 698 bp mRNA linear EST 30-DEC-2003  
BP146990 full-length enriched swine cDNA library, adult ovary Sus  
scrofa cDNA clone OVRM10025B09 5', mRNA sequence.

BP146990.1 GI:40396461

EST.

Sus scrofa (pig)

Sus scrofa

1 (bases 1 to 698)

Uenishi H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamasima, N. and Awata, T.

PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries

Nucleic Acids Res. 32 (1), D484-D488 (2004)

Contact: Hirohide Uenishi  
Animal Genome Laboratory, Genome Research Department  
National Institute of Agrobiological Sciences  
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
Tel: +81-29-838-8627  
Fax: +81-29-838-8627  
Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in  
Animal Genome Research Program (Japan) by National Institute of  
Agrobiological Sciences and STAFF-Institute

Single pass sequencing of clones derived from oligo-capped cDNA  
library

Vector sequences were eliminated by RepeatMasker version 2002/07/13  
and crossmatch version 0.990319

Low quality bases were trimmed based on the quality values.

FEATURES  
Location/Qualifiers  
1..698

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9823"

/clone="OVRM10025B09"

/tissue\_type="ovary"

/dev\_stage="adult"

/clone\_lib="full-length enriched swine cDNA library, adult  
ovary"

Matches 638; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 412 CAGGAGCAGGTTTCATTTTGGAGAGAGGAGGACATATATCTCGAAGCACAAGCCCG 471  
Db 1 CAGGAGCAGGTTTCATTTTGGAGAGAGGAGGACATATATCTCGAAGCACAAGCCCT 60  
Qy 472 TGGATCCCCCAATATACAGTATGCTTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAA 531  
Db 61 TGGATCCCCCAGTTACAGTATGCTTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAA 120  
Qy 532 TATCAGCCTCGAGGGGACTTGTCTACTTTTGAATAGATATAGAGGACCAAGTTAGATGAA 591  
Db 121 TATCAGCCTCGAGGGGACTTGTCTACTTTTGAATAGATATAGAGGACCAATAGATGAA 180  
Qy 592 AACCTGATACAGTTTACCTAGCTAGCTGATTTTGGCTGTTTACAGCGTTTCACTGTATG 651  
Db 181 AATATGATACAGTTTACCTAGCTAGCTGATTTTGGCTGTTTACAGCGTTTCACTGATG 240  
Qy 652 GGATACGTGATCAGACATCAAGCCTGAGAACATCTCTGTTGACCGCACAGGACACATC 711  
Db 241 GGAATGATGATCAGACATCAAGCCTGAGAACATCTCTGTTGACCGCACAGGACACATC 300  
Qy 712 AAGCTGCTGGATTTGGATCTCGCGGAAATGAATTCAAACAGAGATGGTGAATGCCAAA 771  
Db 301 AAGCTGCTGGATTTGGATCTCGCGGAAATGAATTCAAACAGAGATGGTGAATGCCAAA 360  
Qy 772 CTCCCGATTGGAGCCCGAGATTACATGCTTCTGAAGTGTGCTGATGATGAACGGGGAT 831  
Db 361 CTCCCGATTGGAGCCCGAGATTACATGCGCCCTGAAGTGTGCTGATGATGAATGGGGAT 420  
Qy 832 GGAAGAGGACCTTACGCGCTGGACTGTGCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTG 891  
Db 421 GGAAGAGGCTGCTATGCGCTAGACTGTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Qy 892 ATGATTTATGGAGATCCCCCTTGGCAGAGGAACTCTCCGAGAACCTTCAATAACATT 951  
Db 481 ATGATTTATGGAGATCCCCCTTGGCAGAGGAACTCTCCGAGAACCTTCAATAACATC 540  
Qy 952 ATGATTTATGGAGATCCCCCTTGGCAGAGGAACTCTCCGAGAACCTTCAATAACATT 1011  
Db 541 ATGATTTATGGAGATCCCCCTTGGCAGAGGAACTCTCCGAGAACCTTCAATAACATC 600  
Qy 1012 GATCTGATTTCAAGAGCTTTGTTGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1071  
Db 601 GATCTGATTTCAAGAGCTTTGTTGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
Qy 1072 TGGATCTTTCTCTCTAAATGACTGGAAACAAT 1109  
Db 661 TGTCT 698

## RESULT 2

BM904785  
LOCUS  
DEFINITION BM904785 1085 bp mRNA linear EST 12-MAR-2002  
5' mRNA sequence.  
ACCESSION BM904785  
VERSION BM904785.1 GI:19355164  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 1085)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: csapsb@mail.nih.gov  
Tissue Procurement: ATCC/DCTP/DTF  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHAM1279 row: d column: 07  
High quality sequence stop: 510.  
Location/Qualifiers

## FEATURES

## source

1. .1085  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5557590"  
/issue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 72"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 34.4%; Score 521.2; DB 5; Length 1085;  
Best Local Similarity 99.3%; Pred. No. 2.8e-147;  
Matches 534; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 873 GGCGGTGATTGCTATGAGATGATTTATGGAGATCCCTTCGACAGAGGAACTCTGCG 932  
Db 1 GGCGGTGATTGCTATGAGATGATTTATGGAGATCCCTTCGACAGAGGAACTCTGCG 60  
Qy 933 CAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTGTAAATTTCCAGATGACCCCAA 992  
Db 61 CAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTGTAAATTTCCAGATGACCCCAA 120  
Qy 993 AGTGACAGTACTTTCTTGATCTGATCAAAAGCTTTGTGCGGCCAGAAAGAGAGACT 1052  
Db 121 AGTGACAGTACTTTCTTGATCTGATCAAAAGCTTTGTGCGGCCAGAAAGAGAGACT 180  
Qy 1053 GAAGTTTGAAGGCTTTTGTGCTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1112  
Db 181 GAAGTTTGAAGGCTTTTGTGCTGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Qy 1113 TAACT 1172  
Db 241 TAACT 300  
Qy 1173 TGAACACAGAGAGAAATTCGTGGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1232  
Db 301 TGAACACAGAGAGAAATTCGTGGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
Qy 1233 CTGCGGTGAAGAACTGCGGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTGG 1292  
Db 361 CTGCGGTGAAGAACTGCGGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTGG 420  
Qy 1293 TAGATCTGATCTGTTGTGTTGGGTTTGTGGGTTTGTGGGTTTGTGGGTTTGTGGGTT 1352  
Db 421 TAGATCTGATCTGTTGTGTTGGGTTTGTGGGTTTGTGGGTTTGTGGGTTTGTGGGTT 480  
Qy 1353 GAACT 1409  
Db 481 GAACT 538

## RESULT 3

CR746615  
LOCUS  
DEFINITION CR746615 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE0998D012279 ;  
IMAGE:5557590 5', mRNA sequence.  
ACCESSION CR746615  
VERSION CR746615.1 GI:51659741  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;

Db

485 CATGGAAA 492

BG808196 600 bp mRNA linear EST 20-DEC-2001  
2082-86 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,  
mRNA sequence.  
BG808196  
EST. BG808196.1 GI:17955172  
Mus musculus (house mouse)  
Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Mu,X., Zhao,S., Pershad,R., Heieh,T.-F., Scarpa,A., Wang,S.W.,  
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.  
Gene expression in the developing mouse retina by EST sequencing  
and microarray analysis  
Nucleic Acids Res. 29 (24), 4983-4993 (2001)

REFERENCE 1 (bases 1 to 600)  
AUTHORS  
TITLE  
JOURNAL MEDLINE  
PUBMED  
COMMENT

Contact: Klein WH  
Department of Biochemistry and Molecular Biology  
University of Texas M.D. Anderson Cancer Center  
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA  
Tel: 713 792 3646  
Fax: 713 790 0329

Location/Qualifiers  
source  
1..600  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/tissue\_type="neural retina"  
/dev\_stage="embryonic day 14.5 post-fertilization"  
/clone\_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN

Query Match 29.9%; Score 452.8; DB 4; Length 600;  
Best Local Similarity 86.6%; Pred. No. 1.9e-126; Indels 0; Gaps 0;  
Matches 499; Conservative 0; Mismatches 77;

QY 1 GGCGAGATGTGAAGTTCACAAATATGGAGCGCGAATCTTTGGATGTGTGCTGCTGAA 60  
|||  
DB 25 GGAGAGATGTGAAGTTCAGTATGGTGCGGAACCCGCCGAGGCAGTGCCTCCGAG 84  
|||  
QY 61 CCATTGGCAACCGGCGCTCAGGCTGAATCTGTCTTCCAGGGGAAACCAACCTTTATG 120  
|||  
DB 85 CCATTGGCAGTCGGCGCTCCAGGCTTAATCTCTTCTCCAGGGGAAACCGCCCTCATG 144  
|||  
QY 121 ACTCAACGACGATGCTCTCTTCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180  
|||  
DB 145 ACTCAACGACGATGCTCTCTTCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 204  
|||  
QY 181 TTTGAAGATGCAGTCAGCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 240  
|||  
DB 205 TTTGAAGATGCAGCAACCCGCCCTGATGAAGATGAAGCAGTGAAGCAGTTCGTCAG 264  
|||  
QY 241 AAGTATTCGACACCATAGCTGAGTTACAGAGCTTCAGCCTTCGGCAAAGGACTTCGAA 300  
|||  
DB 265 AAGTATTCGACACCATAGCTGAGTTACAGAGCTTCAGCCTTCGGCAAAGGACTTCGAA 324  
|||  
QY 301 GTCAAGTCTGTAGTGTGGTCACTTCTCAAGTGCAGAGTGTGAAGAGAGAACGA 360  
|||  
DB 325 GTTCAAGCCCTGTGGGCTGTGGTCACTTCTCAAGTGCAGAGTGTGAAGAGAGAACGC 384  
|||  
QY 361 ACCGGGACATCTATGCTATGAAGTGTATGAAGAGAGGCTTTATTGGCCCCAGGACAG 420  
|||  
DB 385 ACCGGGACATCTATGCTATGAAGTGTATGAAGAGAGGCTTTATTGGCCCCAGGACAG 444  
|||  
QY 421 GTTTCATTTTTTGGAGAGAGCGGAACAATATTATCTCGAAGCAACAGCCCTGTGATCCCC 480  
|||

```

Db      445 GTTTCATTTTCGAGGAGGAGGAAACATATTATCTCGGAGCAGAGTCCTTGGATCCCC 504
Qy      481 CAATTACAGTATGCTTTTCAGGACAAAATACCTTTATCTGTCATGGAATATCAGCCT 540
Db      505 CAGTTACAGTACGCTTTTCAGGACAAAATAACTTTACCTGCTCATGGAATATCAGCCT 564
Qy      541 GGAGGGGACTTGCTGTCACATTTTCAATAGATATGAG 576
Db      565 GGAGGGGATTGCTGTCGCTTCTGACAGATACGAG 600

RESULT 5
CR746792
LOCUS
DEFINITION CR746792 NCI CGAP Brn64 Homo sapiens cDNA clone IMAGE5998E239412 ;
IMAGE:4149886 5', mRNA sequence.
ACCESSION CR746792
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E.,
Peters, M., Radelof, U. and Schneider, D.
TITLE I.M.A.G.E. cDNA Clone Collection
JOURNAL Unpublished (2004)
COMMENT Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAGE5998E239412.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAAACAGCTATGAC.
FEATURES
source
1..485
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE5998E239412 ; IMAGE:4149886"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (Ti phage-resistant)"
/clone_lib="NCI_CGAP_Brn64"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 28.1%; Score 425.4; DB 7; Length 485;
Best Local Similarity 99.8%; Pred. No. 4.1e-118;
Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGGGAGATGTTGAAGTTCAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA 60
Db      59 GGGGAGATGTTGAAGTTCAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA 118
Qy      61 CCCATTCCCAACCGGGCTCCAGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 120
Db      119 CCCATTCCCAACCGGGCTCCAGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 178
Qy      121 ACTCAACAGCAGATGCTCTCTCTTCCCGAGAGGGATATAGATGCCCTCTTTGTTCTC 180
Db      179 ACTCAACAGCAGATGCTCTCTCTTCCCGAGAGGGATATAGATGCCCTCTTTGTTCTC 238

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```

Qy      181 TTTGAAGATGCACTCAGCTGCTCTGATGAGATTAAACACGCTGAGCACTTTTGTCCG 240
Db      239 TTTGAAGATGCACTCAGCTGCTCTGATGAGATTAAACACGCTGAGCACTTTTGTCCG 298
Qy      241 AAGTATTTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCGCGCAAGAGACTTCGAA 300
Db      299 AAGTATTTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTCGCGCAAGAGACTTCGAA 358
Qy      301 GTCAGAAAGTCTTGAGTTGTGCTCACTTTGCTGAAAGTCAGGTGTAAGAGAGAAAGCA 360
Db      359 GTCAGAAAGTCTTGAGTTGTGCTCACTTTGCTGAAAGTCAGGTGTAAGAGAGAAAGCA 418
Qy      361 ACCGGGGACATCTATCTGATGAAGTATGAGAGAGAGAGCTTTTATGCCCCAGGAGCAG 420
Db      419 ACCGGGGACATCTATCTGATGAAGTATGAGAGAGAGAGCTTTTATGCCCCAGGAGCAG 478
Qy      421 GTTTCAT 427
Db      479 GTTTCAT 485

RESULT 6
BG944539
LOCUS
DEFINITION BG944539 427 bp mRNA linear EST 15-JAN-2003
ax51f11.x2 Hembase; Erythroid Progenitor Cells (LCB:ax library)
Homo sapiens cDNA clone ax51f11 random, mRNA sequence.
ACCESSION BG944539
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Gubin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L.
TITLE Gene expression in proliferating human erythroid cells
JOURNAL Genomics 59 (2), 168-177 (1999)
MEDLINE 99339981
PubMed 10409428
COMMENT Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jm7f@nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 51 row: f column: 11
Seq primer: -21M13 forward primer (ABI).
FEATURES
source
1..427
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ax51f11"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"
/dev_stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
/clone_lib="Hembase; Erythroid Progenitor Cells (LCB:ax library)"
/notes="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;
Site 2: BcoRI; 65,000 proliferating erythroid cells from
the Buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using Trizol reagent. RNA (0.3

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ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOUR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center <http://www.nisc.nih.gov/>).

## ORIGIN

Query Match 28.0%; Score 423.8; DB 4; Length 427;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-117;  
 Matches 425; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 148 CGAAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAAGTCAGCTGCTCTG 207  
 DB 1 CGAAGAGGATATAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAAGTCAGCTGCTCTG 60

QY 208 ATGAAGATTAAAGCACGTGAGCAACTTTGTCGGAAATATTCGACACCATAGCTGAGTTA 267  
 DB 61 ATGAAGATTAAAGCACGTGAGCAACTTTGTCGGAAATATTCGACACCATAGCTGAGTTA 120

QY 268 CAGGAGCTCAGCTTCGCGAAAGACTTCGAAGTCAGAAGTCTTGTAGTGTGTGTCAC 327  
 DB 121 CAGGAGCTCAGCTTCGCGAAAGACTTCGAAGTCAGAAGTCTTGTAGTGTGTGTCAC 180

QY 328 TTGCTGAAGTCAGCTGTAGAGAGAAGCAACCGGGACATCTATGCTATGAAGTG 387  
 DB 181 TTGCTGAAGTCAGCTGTAGAGAGAAGCAACCGGGACATCTATGCTATGAAGTG 240

QY 388 ATGAAGAGAGGCTTTATTTGGCCAGGAGCAGCTTTTCATTTTTCGAGAAAGCGGAAC 447  
 DB 241 ATGAAGAGAGGCTTTATTTGGCCAGGAGCAGCTTTTCATTTTTCGAGAAAGCGGAAC 300

QY 448 ATATTATCTGAAGCAACAGCCGTCGATCCCAATTAAGATGATGCTTTTCAGGACAA 507  
 DB 301 ATATTATCTGAAGCAACAGCCGTCGATCCCAATTAAGATGATGCTTTTCAGGACAA 360

QY 508 AATCAGCTTTACTGCTCATGGAATATCAGCTGGAGGGGACTTGTGTCACCTTTGAAT 567  
 DB 361 AATCAGCTTTACTGCTCATGGAATATCAGCTGGAGGGGACTTGTGTCACCTTTGAAT 420

QY 568 AGATATG 574  
 DB 421 AGATATG 427

## RESULT 7

BQ417810 617 bp mRNA linear EST 23-MAY-2002  
 LOCUS ik51b06.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to  
 DEFINITION TR:088937 088937 RHO/RAC-INTERACTING CITRON KINASE SHORT ISOFORM.  
 ; mRNA sequence.

ACCESSION BQ417810

VERSION BQ417810.1 GI:21123011

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 617)

## REFERENCE

## AUTHORS

Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

## TITLE

## JOURNAL

## COMMENT

Unpublished (2000)  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: [dmelton@biohpc.harvard.edu](mailto:dmelton@biohpc.harvard.edu)  
 Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000) Library was constructed by Catherine Lee DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Searce ([mscearce@mail.med.upenn.edu](mailto:mscearce@mail.med.upenn.edu))

Seq primer: -40RP from Gibco

High quality sequence stop: 367.

Location/Qualifiers

## FEATURES

## source

1. .617

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129/Sv x CD1"

/db\_xref="taxon:10090"

/dev\_stage="p.c. 14.5"

/lab\_host="E. coli-DH12S (GIBCO)"

/clone\_lib="Kaestner ngn3 wt"

/note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site\_1:

Not I; Site\_2: Sal I; The library was prepared by

Catherine S. Lee and has not been published. The pancreas

was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,

2000). The cDNA's were prepared with an oligo containing a

NotI site, and SalI linkers were added to the ends. The

inserts were cut with NotI before being cloned into the

NotI-SalI sites in the vectors. This is one of two

libraries, ngn3 wt and ngn3 -/- . The wt library is in

pSPORT1, T7 promoter is 5'."

## ORIGIN

Query Match 27.3%; Score 413.2; DB 5; Length 617;  
 Best Local Similarity 86.1%; Pred. No. 2.4e-114;  
 Matches 457; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1 CGGGAGATGTTCAAGTTTCAATATATGAGCGCGGAATCTTTGGATGCTGTGCTGTGAA 60  
 DB 87 GGAAGATGTTGAGATTTCAGTATGTTGCGGACCCCGGAGGCCAGTGTCTCGAG 146

QY 61 CCCATTGCCAACCGGGCTCCAGGCTGAATCTGTTTCCAGGGGAAACACCCCTTTATG 120  
 DB 147 CCCATTGCCAGTCCGGGCTCCAGGCTAAATCTCTTCTCCAGGGGAAACCGCCCTCATG 206

QY 121 ACTCAACAGCAGATGCTCTCTTTCCCGAGAGGATATTAGATGCCCTCTTGTCTC 180  
 DB 207 ACTCAACAGCAGATGCTCTCTTTCCCGAGAGGATGCTAGACCCCTCTTCTGCTCTC 266

QY 181 TTTGAAGATGCAAGTCAAGCTGCTCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 240  
 DB 267 TTTGAAGATGCAAGTCAAGCTGCTCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCAG 326

QY 241 AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCGAAGGACTTCGAA 300  
 DB 327 AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCGAAGGACTTCGAA 386

QY 301 GTCAGAAGTCTTGTAGTTGCTGCTCACTTTGCTGAAGTCAGGTGCTAGAGAGAAGCA 360  
 DB 387 GTTCAAGGCTTTGTGGGCTGTGGTCACTTCGCTGAAGTCAGGTGCTAGAGAGAAGGCG 446

QY 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAAGGCTTTATTGGCCAGGAGCAG 420  
 DB 447 ACCGGGACATCTATGCTATGAAGTGAAGAGAAGGCTTTATTGGCCAGGAGCAG 506

QY 421 GTTTCATTTTTTGGAGAGAGCGGAACATATTATCTCGAAGCACACAGCCCGTGGATCCCC 480  
 DB 507 GTTTCATTTTTTGGAGAGAGCGGAACATATTATCTCGAAGCACACAGCTCTTGGATCCCC 566

QY 481 CAATTACAGTATGCCCTTTTCAGGACAAAATACCTTTTATCTGTGTCATGAA 531  
 DB 567 CAGTTACAGTATGCCCTTTTCAGGACAAAATACCTTTTATCTGTGTCATGAA 617

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RESULT 8
CN682405
LOCUS
DEFINITION
CN682405 481 bp mRNA linear EST 17-MAY-2004
E0164B04-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low
density) cDNA library (Long) Mus musculus cDNA clone NIA:E0164B04
IMAGE:30782511 5', mRNA sequence.
CN682405
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 481)
Sharov.A.A., Piao.Y., Matoba.R., Dudekula.D.B., Qian.Y.,
VanBuren.V., Falco.G., Martin.P.R., Stagg.C.A., Bassey.U.C.,
Wang.Y., Carter.M.G., Hamatani.T., Aiba.K., Akutsu.H., Sharova.L.,
Tanaka.T.S., Kimber.W.L., Yoshikawa.T., Jaradat.S.A., Pantano.S.,
Nagaraja.R., Boheler.K.R., Taub.D., Hodes.R.J., Longo.D.L.,
Schlessinger.D., Keller.J., Klotz.E., Kelsoe.G., Umezawa.A.,
Vescovi.A.L., Rossant.J., Kunath.T., Hogan.B.L., Curci.A.,
D'Urso.M., Kelso.J., Hide.W. and Ko.M.S.
Transcriptome analysis of mouse stem cells and early embryos
PLOS Biol. 1 (3), 410-419 (2003)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cnaelgaun.grc.nia.nih.gov
Plate: E0164 row: B column: 04
Seq primer: M13 Reverse
High quality sequence stop: 481
POLYA-No.

FEATURES
source
1. 481
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/EvTac"
/db_xref="niaEST:E0164B04-5"
/db_xref="taxon:10090"
/clone="NIA:E0164B04 IMAGE:30782511"
/sex="Male"
/tissue_type="Embryonic Stem Cell"
/cell_line="129.3 ES cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48
h, low density) cDNA library (Long)"
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES
cells were plated at density 3x103/cm2, on gelatin-coated
plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture
medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,
0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM
beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml
streptomycin. Double-stranded cDNAs were synthesized with
an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3'] from
2ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker Lu-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The

```

average insert size is about 2.8 kb. The library was constructed by Yulan Piao."

```

ORIGIN
Query Match 25.1%; Score 380; DB 7; Length 481;
Best Local Similarity 88.0%; Pred. No. 3.2e-104;
Matches 426; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

QY 297 CGAAGTCAGAGTCTTGTAGGTGCTGCTCATTGCTGAAGTCAGGCTGTTAGAGAGAA 356
Db 1 CGAAGTTCGAAGCCTTGTGGCTGTGCTCATTGCTGAAGTCAGGCTGTTAGAGAGAA 60
QY 357 AGCAACCGGGGACATCTATGCTATGAAGTGAAGAGAGAGCTTTATTGCCCCAGGA 416
Db 61 GGGACCGGGGAGCTCTATGCCATGAATCATGAAGAGAGAGCTTTGCTGCCCCAGGA 120
QY 417 GCAGGTTCATTTTTTGGAGAGAGCGGAGCAATATTATCTCGAAGCACACAGCCCGTGGAT 476
Db 121 ACAGGTTCATTTTTTGGAGAGAGCGGAGCAATATTATCTCGGAGCACAGGTCCTTGGAT 180
QY 477 CCCCCAATTACAGTATGCCCTTTTCAGACAAAATACCTTTATCTGCTCATGGAATATCA 536
Db 181 CCCCCAGTTACAGTATGCCCTTTTCAGACAAAATACCTTTATCTGCTCATGGAATATCA 240
QY 537 GCCTGAGGGGACTTCGCTGCTCACTTTTGAATAGATATGAGGACCACTTAGATCAAAACCT 596
Db 241 GCCTGAGGGGATTTGCTGCTGCTTCTGAACAGATAGAGGACCAATTAGATGAGAGCAT 300
QY 597 GATACAGTTTTTACCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGATA 656
Db 301 GATCCAGTTTTTACCTTGTGCTGAGCTGATTTTGGCTGTTCCACAGCGTGCACCATGGATA 360
QY 657 CGTGCATCAGACATCAAGCCTGAGAACATTTCTGTTGACCGGACAGGACACATCAAGCT 716
Db 361 TGTGCATCAGACATCAAGCCTGAGAACATTTCTGTTGACCGGACAGGACACATCAAGCT 420
QY 717 GGTGGATTTTGGATCTGCCGCAAAATGAATTCACAAAGATGGTGAATGCCAACTCCC 776
Db 421 GGTGGATTTTGGATCGAGCGCTAAGATGAATTCAAATTA---GGTGAATGCCAACTCCC 477
QY 777 GATT 780
Db 478 CATT 481

RESULT 9
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LOCUS
DEFINITION
CN678533 479 bp mRNA linear EST 17-MAY-2004
E0112C12-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low
density) cDNA library (Long) Mus musculus cDNA clone NIA:E0112C12
IMAGE:3077539 5', mRNA sequence.
CN678533
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 479)
Sharov.A.A., Piao.Y., Matoba.R., Dudekula.D.B., Qian.Y.,
VanBuren.V., Falco.G., Martin.P.R., Stagg.C.A., Bassey.U.C.,
Wang.Y., Carter.M.G., Hamatani.T., Aiba.K., Akutsu.H., Sharova.L.,
Tanaka.T.S., Kimber.W.L., Yoshikawa.T., Jaradat.S.A., Pantano.S.,
Nagaraja.R., Boheler.K.R., Taub.D., Hodes.R.J., Longo.D.L.,
Schlessinger.D., Keller.J., Klotz.E., Kelsoe.G., Umezawa.A.,
Vescovi.A.L., Rossant.J., Kunath.T., Hogan.B.L., Curci.A.,
D'Urso.M., Kelso.J., Hide.W. and Ko.M.S.
Transcriptome analysis of mouse stem cells and early embryos
PLOS Biol. 1 (3), 410-419 (2003)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

```



	Best Local Similarity	85.6%;	Pred. No. 1.8e-95;	
	Matches	391;	Conservative	0; Mismatches 66; Indels 0; Gaps 0;
Qy	1	GGGAGAGATGTTGAAGTTC	CAAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCCTGAA	60
Db	34	GGAGAGATGTTGAAGTTC	CAAGTAGTAGTAGCGGAACCGTCCGAGGCCAGTGCCCCCGAG	93
Qy	61	CCCATGCCAAACCGGGCTC	CCAGCTGAAATCTGTTCCTCCAGGGGAAACCAACCTTTATG	120
Db	94	CCCATGCCAGTCGGGCTC	CCAGCTAAATCTCTTCTTCCAGGGGAAACCGCCCTCATG	153
Qy	121	ACTCAACAGCAGATGTCCT	CTCTTCCGGAGAGGGATATTAGATGCCCTTTGTGTTCTC	180
Db	154	ACTCAACAGCAGATGTC	CTCTTCTTCCGGAGAGGGGTGTAGATGCCCTTTGTGTTCTC	213
Qy	181	TTTGAAGATGCACTCAGCT	CGCTCTCATGAAGATTAAGCACGTGAGCAACTTTGTCCGG	240
Db	214	TTGGAAGATGCACTCAGCT	CGCTCATGAGATTAAGCACGTGAGCACTTGTCCGG	273
Qy	241	AAGTATTCGCACACCATAG	CTGAGTTACAGAGCTCCAGCTTCGGCAAAAGGACTTCGAA	300
Db	274	AAGTATTCGCACAGTAGC	AGCTTTACGGGAGCTCCAGCGTCGGTGAAGGACTTCGAA	333
Qy	301	GTCAAGAGTCTGTAGGCTG	TGGTGCACCTTGTGAAGTCGAGGTGTAAGAGAGAAAGCA	360
Db	334	GTGGAAGTCTGTGGGCTG	CGGTGCATTCGCCGAAGTCGAGGTGTAGAGAGAAGGCC	393
Qy	361	ACCGGGGACATCTATGCT	ATATGAAAGTATGAAGAAGAGGCTTTATTTGGCCCGAGGACAG	420
Db	394	ACCGGGGATGCTACGCC	ATCATGAGNAAGCGCGCTTTTCGGGCCCGAGGACAG	453
Qy	421	GTTCATTTTTTGAGGAAG	CGCGAAACATATATATCTC	457
Db	454	GTTCATTTTTTCAGAGG	AGGAGAAACATATATATCC	490

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RESULT 11
BI654262
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI654262      821 bp      mRNA      linear      EST 12-SEP-2001
603280370F01 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5310496 5';
mRNA sequence.
BI654262
BI654262.1 GI:15568498
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 821)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11786 row: 1 column: 17
High quality sequence stop: 648.
Location/Qualifiers
1. 821
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:5310496"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
FEATURES
source

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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam4"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site.1: Sali;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Purth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
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ORIGIN

Query Match	22.7%;	Score 344.2;	DB 4;	Length 821;
Best Local Similarity	84.5%;	Pred. No. 3.5e-93;		
Matches 469;	Conservative	0;	Mismatches 78;	Indels 8; Gaps 7;

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QY 1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGCTGTCTGTGAA 60
DB 101 GGAGAGATGTTGAAGTTCAAGTATGGTGTGCGGAACCCGCCGAGGCCAGTGTCTCGAG 160
QY 61 CCATTGCCAACCGGGCTCCAGGCTGAATCTCTTCCAGGGGAAACACACCTTTATG 120
DB 161 CCCATTGCCAGTCGGGCTCCAGGCTAAATCTCTTCCAGGGGAAACACGCCCTCATG 220
QY 121 ACTCAACAGCAGATGCTCCTCTTCCGAGAGAGGATATAGATGCCCTCTTTGTTCTC 180
DB 221 ACTCAACAGCAGATGCTCTCTTTCCCGGAAAGGATGCTAGACGCCCTCTTCGCTCTC 280
QY 181 TTTGAAGATGCACTCAGCTCCTCTGATGAAGATTAAAGCACCTGAGCAACTTTGTCCGG 240
DB 281 TTGGAAGATGTCAGCCAAACCCGCCCTGATGAAGATGAGCATGTAGAGCTTAGTCCAG 340
QY 241 AGTATTCCGACACCATAG-CTGAGTTACAGGAGCTCCAGCCTTCGGCAAGACATTCGA 299
DB 341 AGTATTCCGACACCATAGGCCGAGTTGCGGAGCTGCAGCCGTCGCGGAGAGACTTCGA 400
QY 300 A-CTCAGAGTCTGTAGTTGTGGTCACTTTTCTGCTGAGTGCAGAGTGG-TAAGAGAGAA 357
DB 401 AGGTTCGAAGCCTTGTGGGCTGTGGTCACTTCCTGCAAGTGCAGGTGGTTACGAGAGA 460
QY 358 GC AACCGGGGACATCTATGCTATGAAGTATGA-AGAAGAAGGCTTTATTTGGCCCAAG 416
DB 461 GCAGCCGGGACGCTATGCCATGAANAATCATGACAGAGAAGGCTTTGTCGGCCCAAG 520
QY 417 GCAGGTTTCATTTTTTGAGGAAGCGGAA-CATATTATCTGAAGCACAAAGCCCGTGG 475
DB 521 ACAGGTTTCATTTTTTCGAGGAGAGAGAACCATATTATCTCGAGCACAGTCTCTGGA 580
QY 476 TCCCCCAATTACAGTATGCTTTTCAGGA-CAAAAATACCTTTATCTGCTCATGG--AAT 532
DB 581 TCACCAAGTTTACAGTATGCGCTTTTCAGGACCAAAAAATAAACTTTTACCTGGTTCATGG 640
QY 533 ATCAGCCTGGAGGG 547
DB 641 ATCAGCCTGGATGG 655
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RESULT 12

CG501400

LOCUS

DEFINITION

OST45250 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST45250, mRNA sequence.

ACCESSION

VERSION

CG501400

KEYWORDS

CG501400.1 GI:37275069

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 450)

Zambrowicz, B.P., Abuln, A., Ramirez-Solis, R., Richter, L.J., Piggett, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, J., Shaw, J., Schrick, J., Shi, Z.-Z.,



Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C. and Sands, A.T.  
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
Contact: Zambrowicz BP  
Omnibank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

## FEATURES

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129SV/Ev"  
/db\_xref="taxon:10090"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129SV/Ev"

## ORIGIN

Query Match 21.7%; Score 329.2; DB 9; Length 450;  
Best Local Similarity 90.0%; Pred. No. 1.1e-88;  
Matches 352; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
QY 1124 CCCCCTTGGTCCACGCTCAAGTCGACGATGACACCTCCAAATTTTGATGAACACGAGA 1183  
DB 2 CCCCCTTGGTCCACGCTCAAGTCGACGATGACACCTCCAAATTTTGATGAACACGAGA 61  
QY 1184 AGAATTCGTGGGTTTATCTCTCCGTCGCGAGTCGACGCTCCAGGCTCTCGGGTGAAG 1243  
DB 62 AGAATTCGTGGGTTTATCTCTCTGTGTCGACGTCGACGCTCCAGGCTCTCGGGGAG 121  
QY 1244 AACTGCCGTTTGTGGGTTTTCGTACAGCAAGCACTGGGGATCTTGGTAGATCTGAGT 1303  
DB 122 AGCTGCGTTTGTGGGATTTTGTACAGCAAGCACTGGGGATCTTGGTAGATCTGAGT 181  
QY 1304 CTGTTGTGGGTCGTGGACTCCCTGCGAAGTCTCAGTCTCCATGGAAGAACTCTCA 1363  
DB 182 CTGTCGTGTGAGTCTGGACTCCCTGCCAAGTGTAGCTCCATGGAAGAACTCTCA 241  
QY 1364 TCAAAAGCAAGAGCTACAGACTCTCAGCAAGGTGTCAAGGTATTTATTTCCGCGAG 1423  
DB 242 TCAAAAGCAAGAGCTCAAGACTCCAGCAAGGTGTCAAGGTATCTATCTCCACAG 301  
QY 1424 CCGGCTCTCTTCTTGTCTCAGGATCTCCCGTCCGTATATGCAAGGGATCCGCGGG 1483  
DB 302 CCGGCTCTCTTCTTGTCTCAGGATCTCCCGTCCGTATATGCAAGGGATCTGCGGG 361  
QY 1484 GCGCTGTGGTCTGAGCGGCTGATCGT 1514  
DB 362 GCCACTGCTTGANCCGTGGTGGTCCCTCCCT 392

## RESULT 13

BF344814 423 bp mRNA linear EST 22-NOV-2000  
LOCUS 602014091F1 NCI CGAP\_Brn64 Homo sapiens cDNA clone IMAGE:4149886  
5', mRNA sequence.

ACCESSION BF344814  
VERSION BF344814.1 GI:11292270

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 423)  
NIF-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9412 row: e column: 23  
High quality sequence stop: 423.  
Location/Qualifiers  
1..423

## FEATURES

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/clone\_lib="NCI CGAP\_Brn64"  
/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.57 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 21.7%; Score 328.8; DB 2; Length 423;  
Best Local Similarity 95.7%; Pred. No. 1.4e-88;  
Matches 360; Conservative 0; Mismatches 12; Indels 4; Gaps 2;  
QY 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCTTCGGATGCTGGTCTGCTGAA 60  
DB 48 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCTTCGGATGCTGGTCTGCTGAA 107  
QY 61 CCCATTGCCAACCGGGCTCCAGGCTGAATCTGTTCCAGGGGAACACCCCTTTATG 120  
DB 108 CCCATTGCCAGCGGGCTCCAGGCTGAATCTGTTCCAGGGGAACACCCCTTTATG 167  
QY 121 ACTCAACAGCAGATGTCCTCTTTCCGAGAGGATATTAGATGCCCTCTTTGTTCTC 180  
DB 168 ACTCAACAGCAGATGTCCTCTTTCCGAGAGGATATTAGATGCCCTCTTTGTTCTC 227  
QY 181 TTTGAAGAAATGCAGTCAGCTGCTCTG--ATGAAGATTAAAGCACGTG--AGCAACTTTGT 236  
DB 228 TTTGAAGAAATGCAGTCAGCTGCTCTGTCATGCAAGATTAAAGCACGTGCAACCTTTGT 287  
QY 237 CGGAGATGATTCGACACCATAGCTAGTTACAGGAGCTCCAGCTTCGGAAGGACTT 296  
DB 288 CCGGAAGTATTCGACACCATAGCTAGTTACAGGAGCTCCAGCTTCGGAAGGACTT 347  
QY 297 CGAAGTCAAGTCTTTGTAGTGTGTCATCTTTGCTGAAGTCAGTGGTAAAGAGAGAA 356  
DB 348 CGAAGTCAAGTCTTTGTAGTGTGTCATCTTTGCTGAAGTCAGTGGTAAAGAGAGAC 407  
QY 357 AGCAACCGGGACATC 372  
DB 408 AGCAACCGGGACATC 423

## RESULT 14

CG501399  
LOCUS CG501399  
DEFINITION OST45249 Mus musculus 129SV/Ev Mus musculus cDNA clone OST45249,  
mRNA sequence.

ACCESSION CG501399

VERSION CG501399.1 GI:37275067

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 449)  
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.  
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 Contact: Zambrowicz BP  
 OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: materials@lexgen.com  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
 Class: Gene Trap.

FEATURES  
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 1. .449  
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 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 21.6%; Score 327; DB 9; Length 449;  
 Best Local Similarity 91.8%; Pred. No. 5.1e-88;  
 Matches 345; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
 QY 1118 CTCTCCCTCCCTTCGTTCCACCTCAAGTCCGACGATGACACCTCCAAATTTTGATGAAC 1177  
 Db 6 CTCCTCCCTCCCTTCGTTCCACCTCAAGTCCGACGATGACACCTCCAAATTTTGATGAAC 65  
 QY 1178 CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCAGCTGAGCCCTCAGGCTTCCTCGG 1237  
 Db 66 CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCAGCTGAGCCCTCAGGCTTCCTCGG 125  
 QY 1238 GTGAAGAACTCCGCTTTGTGGGTTTCGTACAGCAAGGCACTGGGGATTCCTGGTAGAT 1297  
 Db 126 GCGAAGAGCTCCGCTTTGTGGGTTTCGTACAGCAAGGCACTGGGGATTCCTGGTAGAT 185  
 QY 1298 CTGAGTCTGTGTGTCGGGTCTGGACTCCCTGCGAAGACTAGCTCCATGAAAGAAC 1357  
 Db 186 CTGAGTCTGTGTGTCGGGTCTGGACTCCCTGCGAAGACTAGCTCCATGAAAGAAC 245  
 QY 1358 TTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACAAAGTGTCAAGGTATTTATTT 1417  
 Db 246 TTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACAAAGTGTCAAGGTATTTATTT 305  
 QY 1418 CCGCAGCCGGCTCTCTTCCTTGTCTCCAGGATCTCTCCGTCGCTATATGCAAGGGATCCG 1477  
 Db 306 CCACAGCCGGCTCTCTTCCTTGTCTCCAGGATCTCTCCAGTCAATATATGCCAGGGATCTG 365  
 QY 1478 CCGGGGCCCTGCTGCT 1493  
 Db 366 CCGGGGCCCTGCTGCT 381

## RESULT 15

CG652891  
 LOCUS OST417039 Mus musculus 129Sv/Ev Mus musculus cdna clone OST417039, mRNA sequence.  
 DEFINITION  
 CG652891  
 ACCESSION  
 CG652891.1 GI:37476740  
 VERSION  
 GSS.  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 512)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.  
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 Contact: Zambrowicz BP  
 OmniBank

## TITLE

## JOURNAL

## COMMENT

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
 Class: Gene Trap.

## FEATURES

## source

Location/Qualifiers  
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 /clone="OST417039"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

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 Best Local Similarity 92.0%; Pred. No. 2.6e-85;  
 Matches 346; Conservative 0; Mismatches 29; Indels 1; Gaps 1;  
 QY 1118 CTCTCCCTCCCTTCGTTCCACCTCAAGTCCGACGATGACACCTCCAAATTTTGATGAAC 1177  
 Db 8 CTCCTCCCTCCCTTCG-TCCCNCTCAAGTCTGACGATGACACCTCCAAATTTTGATGAAC 66  
 QY 1178 CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCAGCTGAGCCCTCAGGCTTCCTCGG 1237  
 Db 67 CAGAGAAGAAATTCGTGGGTTTCATCTCTGTGTGCCAGCTGAGCCCTCAGGCTTCCTCG 126  
 QY 1238 GTGAAGAACTCCGCTTTGTGGGTTTCGTACAGCAAGGCACTGGGGATTCCTGGTAGAT 1297  
 Db 127 GCGAAGAGCTCCGCTTTGTGGGATTTTCGTACAGCAAGGCACTGGGGATTCCTGGTAGAT 186  
 QY 1298 CTGAGTCTGTGTGTCGGGTCTGGACTCCCTGCGAAGACTAGCTCCATGAAAGAAC 1357  
 Db 187 CTGAGTCTGTGTGTCGGGTCTGGACTCCCTGCGAAGACTAGCTCCATGAAAGAAC 246  
 QY 1358 TTCTCATCAAAAGCAAGAGCTACAAGACTCTCAGGACAAAGTGTCAAGGTATTTATTT 1417  
 Db 247 TTCTCATCAAAAGCAAGAGCTCCAAGACTCCCGAGCAAGTGTCAAGGTATTTATTT 306  
 QY 1418 CCGCAGCCGGCTCTCTTCCTTGTCTCCAGGATCTCTCCGTCGCTATATGCAAGGGATCCG 1477  
 Db 307 CCACAGCCGGCTCTCTTCCTTGTCTCCAGGATCTCTCCAGTCAATATATGCCAGGGATCTG 366  
 QY 1478 CCGGGGCCCTGCTGCTG 1493  
 Db 367 CCGGGGCCCTGCTGCT 382

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 Job time : 4599.53 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 06:24:41 ; Search time 767.108 Seconds  
(without alignments)  
11691.196 Million cell updates/sec

Title: US-10-724-594-1

Perfect score: 1515

Sequence: 1 ggggagatgttgagttca.....tctgagccgcgtgacgta 1515

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1515	100.0	1515	8 ACA61394	ACA61394 cDNA enco
2	1515	100.0	1515	10 AAD59938	Aad59938 Human kin
3	1515	100.0	1515	12 ADO40591	Ado40591 Human kin
4	1510.2	99.7	2066	6 AAD26454	Aad26454 Human kin
5	1505.8	99.4	1785	10 AB268726	Abz68726 Nucleotid
6	1481.8	97.8	1485	10 AB268725	Abz68725 Nucleotid
7	1404.2	92.7	6298	6 AAD38864	Aad38864 Human kin
8	1398.2	92.3	1870	8 ADA05643	Ada05643 Human NOV
9	1398.2	92.3	5877	6 ABQ78871	Abq78871 Human kin
10	1398.2	92.3	6156	9 AAL55217	Aal55217 Human CRI
11	1398.2	92.3	6165	6 ABQ78870	Abq78870 Human kin
12	1398.2	92.3	6165	9 AAL55214	Aal55214 Human CRI
13	1398.2	92.3	8603	9 AAL55215	Aal55215 Human CRI
14	1397.8	92.3	6574	6 AAD39191	Aad39191 Human MDP
15	1397.8	92.3	6574	10 ADP60992	Adf60992 Pain asso
16	1397.8	92.3	6574	13 ADQ89099	Adq89099 Human uro
17	1395	92.1	1870	12 ADM62808	Adm62808 Human NOV
18	1391.8	91.9	6162	10 ADF60993	Adf60993 ORF of pa
19	1388	91.6	8656	12 ADJ96544	Adj96544 Human cit
20	1382	91.2	6159	4 AAS06701	Aas06701 Polynucle

21	1375.8	90.8	6189	6 ABS63436	Abs63436 RHQ/RAC-1
22	1375.8	90.8	6189	8 ADA05641	Ada05641 Human NOV
23	1375.8	90.8	6189	12 ADM62806	Adm62806 Human NOV
24	1375.8	90.8	6201	6 ABS63435	Abs63435 Human cDN
25	1375.8	90.8	6201	8 ADA05653	Ada05653 Human NOV
26	1375.8	90.8	6201	12 ADM62818	Adm62818 Human NOV
27	1158	76.4	2380	10 ABZ68776	Abz68776 Nucleotid
28	963.2	63.6	2162	8 ABX71191	Abx71191 Novel hum
29	955.4	63.1	957	11 ADM62729	Adm62729 Human cit
30	940.8	62.1	1048	5 AAS79753	Aas79753 DNA encod
31	760.8	50.2	1133	10 ADJ79946	Adj79946 Human kin
C	578.8	38.2	2896	5 ABV30132	Abv30132 Human pro
C	441.8	29.2	446	5 ABV15823	Abv15823 Human pro
C	434.4	28.7	485	5 ABV45624	Abv45624 Human pro
35	247.2	16.3	3835	8 ABT33346	Abt33346 NOYX DNA
36	247.2	16.3	3985	8 ABT33347	Abt33347 NOYX DNA
37	246.8	16.3	1530	6 AAD38845	Aad38845 Human kin
38	246.8	16.3	4698	12 ADP47966	Adp47966 Human MRC
39	246.8	16.3	4707	12 ADF95101	Adf95101 Human ser
40	246.8	16.3	4944	12 ADF95099	Adf95099 Human ser
41	246.8	16.3	5373	6 AAD30567	Aad30567 Human kin
42	246.8	16.3	5373	12 ADQ15093	Adq15093 Human can
43	246.8	16.3	5438	12 ADJ96545	Adj96545 Human dys
44	246.8	16.3	5619	12 ADI40903	Adi40903 Human kin
45	246.8	16.3	5973	10 ADC99116	Adc99116 Human KPP

ALIGNMENTS

RESULT 1  
ACA61394  
ID ACA61394 standard; cDNA; 1515 BP.  
XX  
AC ACA61394;

DT 11-AUG-2003 (first entry)  
XX  
DE cDNA encoding novel human kinase.

KW Human; ss; gene; gene therapy; kinase; antisense.  
XX  
OS Homo sapiens.

FH Key Location/Qualifiers  
FT 5'UTR 1..6  
FT CDS /\*tag= a  
FT CDS 7..1500  
FT /\*tag= b  
FT /\*product= "Kinase"  
FT 3'UTR 1501..1515  
FT /\*tag= c

XX US2003022340-A1.

XX 30-JAN-2003.

XX 11-SEP-2002; 2002US-00238709.

XX 13-MAR-2001; 2001US-00804471.

XX (APPL-) APPLERA CORP.

XX Webster M, Yan C, Di Francesco V, Beasley EM;

XX WPI; 2003-438978/41.

XX P-PSDB; ABU10126.

XX New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression.

PS Claim 4; Fig 1; 207pp; English.

XX The invention relates to a novel isolated human kinase. The kinase  
 CC peptides and nucleic acids are useful as models for the development of  
 CC human therapeutic targets, in the identification of therapeutic proteins,  
 CC and serve as targets for the development of human therapeutic agents that  
 CC modulate kinase activity in cells and tissues that express the kinase.  
 CC The proteins can be used to raise or to elicit another immune response,  
 CC as a reagent in assays designed to determine the levels of the protein in  
 CC biological fluids, as markers for tissue in which the corresponding  
 CC protein is preferentially expressed, in the identification of modulators  
 CC of the peptides and in pharmacogenomic analysis. The nucleic acids are  
 CC useful as hybridisation probes, in constructing vectors, host cells or  
 CC transgenic animals expressing all or a part of the nucleic acid, for  
 CC monitoring the effectiveness of modulating compounds on the expression or  
 CC activity of the transporter gene in clinical trials or in treatment  
 CC regimen, in gene therapy and as antisense constructs to control  
 CC transporter gene expression in cells, tissue and organisms. The present  
 CC sequence represents a novel human kinase

XX Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

Query Match 100.0%; Score 1515; DB 8; Length 1515;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGAA 60  
 DB 1 GGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGAA 60  
 QY 61 CCATATGCCAACCGGGCTCCAGCTGAATCTGTTCTCCAGGGGAAACCACTTTATG 120  
 DB 61 CCATATGCCAACCGGGCTCCAGCTGAATCTGTTCTCCAGGGGAAACCACTTTATG 120  
 QY 121 ACTCAACAGCAGATGCTCCTCTTTCCGAGAGGGATATAGATGCCCTCTTTGTTCTC 180  
 DB 121 ACTCAACAGCAGATGCTCCTCTTTCCGAGAGGGATATAGATGCCCTCTTTGTTCTC 180  
 QY 181 TTGAGAAATGCAGTACGCTGCTCTGATGAAGTTAAGCAGCTGAGCACTTTGTCGG 240  
 DB 181 TTGAGAAATGCAGTACGCTGCTCTGATGAAGTTAAGCAGCTGAGCACTTTGTCGG 240  
 QY 241 AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGGCTTCGGCAAGAGACTTCGAA 300  
 DB 241 AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGGCTTCGGCAAGAGACTTCGAA 300  
 QY 301 GTCAGAGTCTTGTAGTGTGCTCACTTTGCTGAAGTCAAGTGGTGAAGAGAAAGCA 360  
 DB 301 GTCAGAGTCTTGTAGTGTGCTCACTTTGCTGAAGTCAAGTGGTGAAGAGAAAGCA 360  
 QY 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 DB 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 QY 421 GTTTTCATTTTGGAG 480  
 DB 421 GTTTTCATTTTGGAG 480  
 QY 481 CAATACAGTATGCTTTTCAGGACAAATATCACTTTATCTGTTATGGAATATCAGCCT 540  
 DB 481 CAATACAGTATGCTTTTCAGGACAAATATCACTTTATCTGTTATGGAATATCAGCCT 540  
 QY 541 GGAGGGACCTGCTGCTCACTTTTGAATAGATAGAGAGAGAGAGAGAGAGAGAGAG 600  
 DB 541 GGAGGGACCTGCTGCTCACTTTTGAATAGATAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 601 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTTCAACAGCGTTTCTCTGATGGATAGTG 660  
 DB 601 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTTCAACAGCGTTTCTCTGATGGATAGTG 660  
 QY 661 CATCGAGACATCAAGCTGAGAAATCTCTGTTGACCGGACAGGACATCAAGCTGGTG 720  
 DB 661 CATCGAGACATCAAGCTGAGAAATCTCTGTTGACCGGACAGGACATCAAGCTGGTG 720

QY 721 GATTTGGATCTGCGCGAAATGAATTCAAACAAGATGATGAATGCGCAAACTCCCGATT 780  
 DB 721 GATTTGGATCTGCGCGAAATGAATTCAAACAAGATGATGAATGCGCAAACTCCCGATT 780  
 QY 781 GGGACCCAGATTTACATGCTCTCTGAAGTCTGACTGTGATGAACGGGATGAAAGGC 840  
 DB 781 GGGACCCAGATTTACATGCTCTCTGAAGTCTGACTGTGATGAACGGGATGAAAGGC 840  
 QY 841 ACCTACGGCTGAGCTGACTGTGCTGCTGAGTGGGCTGATTCCTATGAGATGATTAT 900  
 DB 841 ACCTACGGCTGAGCTGACTGTGCTGCTGAGTGGGCTGATTCCTATGAGATGATTAT 900  
 QY 901 GGGAGATCCCTCTTCGACAGAGGAACTCTGCCAGAACCTTCAATAACATTATGAATTC 960  
 DB 901 GGGAGATCCCTCTTCGACAGAGGAACTCTGCCAGAACCTTCAATAACATTATGAATTC 960  
 QY 961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTTTGTGATGATT 1020  
 DB 961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTTTGTGATGATT 1020  
 QY 1021 CAAAGCTTGTGTCGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCT 1080  
 DB 1021 CAAAGCTTGTGTCGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCT 1080  
 QY 1081 TTCTTCTTAAATTTGACATGGAACAACTCTCTCTCCCTCCCTCTCGTTCCCACT 1140  
 DB 1081 TTCTTCTTAAATTTGACATGGAACAACTCTCTCTCCCTCCCTCTCGTTCCCACT 1140  
 QY 1141 CTCAAGTCCGACGATGACACTCTCAATTTTGTATGAACAGAGAGAAATTCGTGGTTCA 1200  
 DB 1141 CTCAAGTCCGACGATGACACTCTCAATTTTGTATGAACAGAGAGAAATTCGTGGTTCA 1200  
 QY 1201 TCCTCTCGCTGACGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTGTTGGG 1260  
 DB 1201 TCCTCTCGCTGACGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTGTTGGG 1260  
 QY 1261 TTTTCGTACAGCAAGCACTGGGGATTTGTTGTAGATCTGAGTCTGTTGTGCGGTTCTG 1320  
 DB 1261 TTTTCGTACAGCAAGCACTGGGGATTTGTTGTAGATCTGAGTCTGTTGTGCGGTTCTG 1320  
 QY 1321 GACTCCCTGCGAAGTACTAGTCCATGGAAGAAATCTTCTATCAAAAGCAAGAGCTA 1380  
 DB 1321 GACTCCCTGCGAAGTACTAGTCCATGGAAGAAATCTTCTATCAAAAGCAAGAGCTA 1380  
 QY 1381 CAGAGCTCTCAGCAAGTGTCAAGGTAATTTATTTCCGACCGCGCTCTTCTCTGTC 1440  
 DB 1381 CAGAGCTCTCAGCAAGTGTCAAGGTAATTTATTTCCGACCGCGCTCTTCTCTGTC 1440  
 QY 1441 TCCAGGATCTCCCGTCCGTATATGCAAGGATCCGCGCGGCGCTCTGCTGCTGA 1500  
 DB 1441 TCCAGGATCTCCCGTCCGTATATGCAAGGATCCGCGCGGCGCTCTGCTGCTGA 1500  
 QY 1501 GCCGCTGATCCGTA 1515  
 DB 1501 GCCGCTGATCCGTA 1515

RESULT 2

AAD5938  
 ID AAD5938 standard; cDNA; 1515 BP.

XX AAD5938;

XX AC AAD5938;

XX 18-DEC-2003 (first entry)

XX Human kinase cDNA.

XX Human; kinase protein; diagnostic; therapeutic; immune response;

XX pharmacogenomic; tissue typing; gene therapy; chromosome 12; transgenic;

XX gene; ss.

XX Homo sapiens.



Db	1321	GACTCCCTGCCAAGACTAGCTCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTA	1380
Qy	1381	CAAGACTCTCAGGACAAGTGTCAACAAGTATTTATTTCCGACGCGGCCCTCTTCCCTTGC	1440
Db	1381	CAAGACTCTCAGGACAAGTGTCAACAAGTATTTATTTCCGACGCGGCCCTCTTCCCTTGC	1440
Qy	1441	TCCAGGATCTCCCGTCCGTATATGCAAGGGATCCGCCGGGGCCGCTCTGGCTCTGA	1500
Db	1441	TCCAGGATCTCCCGTCCGTATATGCAAGGGATCCGCCGGGGCCGCTCTGGCTCTGA	1500
Qy	1501	GCGCCCTGATCCCGTA	1515
Db	1501	GCGCCCTGATCCCGTA	1515

### RESULT 3

RESUL 3  
ADO40591

ADO40591  
ID ADO40591 standard; cDNA; 1515 BP.

AC ADO40591;

29-JUL-2004 (first entry)

XX DE Human kinase cDNA.

KW rho/rac-interacting citron kinase: drug screening: XX

KW kinase related disorder; human; chromosome 12; gene; ss.  
KW kinase; tmo/tac-interacting cation kinase; drug screening

xx Homo sapiens.

XX	Key	Location/Qualifiers
FH		

FT	key	local
FT	5' UTR	1. .6

FT / \*tag=

FT	CDS	7.15
7.15	7.15	7.15

ET / \*tag=

FT	product= "Human kinase protein"
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EM /4420

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PN  
US2004091993-A1.

XX  
PD  
13-MAY-2004

XX PF 02-DEC-2003: 2003US-00724594.

XX  
PR 13-MAR-2003: 2001US-00804471

PR 13-MAR-2001; 2001US-008044/L.  
PR 11-SEP-2002; 2002US-00238709.

XX PA (APPL-) APPLERA CORP.

XX PI Webster M. Yan C. Di Francesco V. Beasley EM:

XX  
DB WPT: 2004-374957/35

DR WPI; Z004-3/4951/  
DR P-PSDB: ADO40592.

xx New isolated human kinase proteins and nucleic acids, useful for  
 PT developing human therapeutic targets, identifying therapeutic proteins or  
 PT serve as targets for the development of human therapeutic agents that  
 PT modulate kinase activity.

PS Claim 4; SEQ ID NO 1: 207pp; English.

The present invention provides a kinase polypeptide and its encoding polynucleotide. The polypeptide and polynucleotide of the invention are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The invention is also useful for biological assays related to kinases, in drug screening assays, for treating disorders characterized by an absence of inappropriate and unwanted expression of the protein. The present sequence is human kinase cDNA. The human kinase gene is located on chromosome 12.

Qy	1021	CAAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTTGCTGCTCCATCCT	1080
Db	1021	CAAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTTGCTGCTCCATCCT	1080
Qy	1081	TTCTTCTCTAAATTTGACTTGAACCAATTCGTTAACTCTCTCTCCCCCTTTGTTTCCACCC	1140
Db	1081	TTCTTCTCTAAATTTGACTTGAACCAATTCGTTAACTCTCTCTCCCCCTTTGTTTCCACCC	1140
Qy	1141	CTCAAGTCCGACGATGACACCTCCAAATTTTGTGATGAACCCAGAGAAGAAATTCGTGGGTTTCA	1200
Db	1141	CTCAAGTCCGACGATGACACCTCCAAATTTTGTGATGAACCCAGAGAAGAAATTCGTGGGTTTCA	1200
Qy	1201	TCCTTCTCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGCTTTGTGGGG	1260
Db	1201	TCCTTCTCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGCTTTGTGGGG	1260
Qy	1261	TTTTTCGTACAGCAAGGCACCTGGGATTCCTTGGTAGATCTCAGTCTGTGTGTCGGGCTCG	1320
Db	1261	TTTTTCGTACAGCAAGGCACCTGGGATTCCTTGGTAGATCTCAGTCTGTGTGTCGGGCTCG	1320
Qy	1321	GACTCCCTCTGCCAGACTAGCTCCATGGAAAAAGAACTTCTCATCAAAAACAAAGAGCTA	1380
Db	1321	GACTCCCTCTGCCAGACTAGCTCCATGGAAAAAGAACTTCTCATCAAAAACAAAGAGCTA	1380
Qy	1381	CAGACTCTCAGGACAAGTGTCAAGAGTATTTATTTTCGAGCCGCGCTTCTTCTCTTGC	1440
Db	1381	CAGACTCTCAGGACAAGTGTCAAGAGTATTTATTTTCGAGCCGCGCTTCTTCTCTTGC	1440
Qy	1441	TCCAGGATCTCCCGTCCGTATATGCCAAGGATCCGCCCGGGCGCTCTCGCTCTGA	1500
Db	1441	TCCAGGATCTCCCGTCCGTATATGCCAAGGATCCGCCCGGGCGCTCTCGCTCTGA	1500
Qy	1501	GCGCCCTGATCCGTA 1515	
Db	1501	GCGCCCTGATCCGTA 1515	
RESULT 4			
AAAD26454			
ID	AAAD26454	standard; cdna; 2066 BP.	
XX	AC	AAAD26454;	
XX	AC	AAAD26454;	
XX	AC	AAAD26454;	
DT	26-MAR-2002	(first entry)	
XX	Human kinase	PKIN-7 cdna.	
DE	Human kinase	PKIN-7 cdna.	
XX	Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis;		
KW	Human disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;		
KW	Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;		
KW	allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;		
KW	autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis;		
KW	Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;		
KW	rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;		
KW	hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;		
KW	cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;		
KW	congestive heart failure; ischaemic heart disease; lung tumour; gout;		
KW	fatty liver; Niemann-Pick's disease; gene therapy; ss.		
XX	Homo sapiens.		
XX	OS		
XX	Key	Location/Qualifiers	
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FT	FT	/product= "Human PKIN-7 protein"	
XX	XX		
PN	WO200196547-A2.		
XX	XX		
XX	20-DEC-2001.		
PD	PD		
XX	XX		
XX	14-JUN-2001; 2001WO-US019444.		
XX	XX		

PR	15-JUN-2000; 2000US-0212073P.	
PR	23-JUN-2000; 2000US-0213467P.	
PR	30-JUN-2000; 2000US-0215651P.	
PR	07-JUL-2000; 2000US-0216605P.	
PR	13-JUL-2000; 2000US-0218372P.	
PR	25-AUG-2000; 2000US-0228056P.	
XX	(INCY-) INCYTE GENOMICS INC.	
PA		
XX		
PI	Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;	
PI	Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DM, Greenwald SR;	
PI	Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;	
PI	Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;	
PI	Lo TP, Khan F, Recipon SA, Asimzai Y, Policky JB, Ding L;	
PI	Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;	
XX		
XX	WPI: 2002-090207/12.	
DR	P-PSDB; AAE16261.	
DR		
XX		
PT	New polypeptides, useful for diagnosing, treating or preventing disorders	
PT	of growth and development, cardiovascular and lipid, and diseases such as	
PT	cancer, comprise human kinase polypeptides.	
PS		
XX	Claim 5; Page 180-181; 197pp; English.	
XX		
CC	The invention relates to human kinase PKIN proteins and their	
CC	corresponding cDNAs. A composition containing PKIN agonist is useful for	
CC	treating a disease or condition associated with decreased expression of	
CC	PKIN and a composition comprising PKIN antagonist is useful for treating	
CC	a disease or condition associated with overexpression of PKIN. The	
CC	disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,	
CC	myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder	
CC	(Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,	
CC	atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,	
CC	autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes	
CC	mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,	
CC	osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,	
CC	rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,	
CC	bacterial, parasitic, fungal, viral, protozoal and helminthic infections)	
CC	growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,	
CC	Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio	
CC	vascular disease (arteriovenous fistula, hypertension, vasculitis,	
CC	aneurysms, congestive heart failure, angina pectoris, myocarditis,	
CC	ischemic heart disease, chronic bronchitis, lung tumours); lipid	
CC	disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,	
CC	hypercholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity	
CC	of a test compound and in gene therapy. The present sequence is human	
CC	PKIN-7 cDNA	
XX		
SQ	Sequence 2066 BP; 515 A; 497 C; 516 G; 538 T; 0 U; 0 Other;	
	Query Match 99.7%; Score 1510.2; DB 6; Length 2066;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 1512; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Qy	1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA 60	
Db	8 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA 67	
Qy	61 CCATTGCCAACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATG 120	
Db	68 CCATTGCCAGCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATG 127	
Qy	121 ACTCAACGAGATGTCCTCTCTTCCGAGAGGGATATAGATGCCCTCTTTGTTCTC 180	
Db	128 ACTCAACGAGATGTCCTCTCTTCCGAGAGGGATATAGATGCCCTCTTTGTTCTC 187	
Qy	181 TTTGAAGATGCACTCAGCTGCTCTGATGAAGATTAAGCACTGAGCAACTTTGTCGG 240	
Db	188 TTTGAAGATGCACTCAGCTGCTCTGATGAAGATTAAGCACTGAGCAACTTTGTCGG 247	
Qy	241 AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGCGAAAGGACTTCGAA 300	

248 AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAA 307  
301 GTCAAGAGTCTTGAGTGTGGTGCACCTTGCTCAAGTGCAGGTGGTAAGAGAAAGCA 360  
308 GTCAAGAGTCTTGAGTGTGGTGCACCTTGCTCAAGTGCAGGTGGTAAGAGAAAGCA 367  
361 ACCGGGACATCTATGCTATGAAAGTGTATGAAGAAAGGCTTTATTTGGCCAGGAGCAG 420  
368 ACCGGGACATCTATGCTATGAAAGTGTATGAAGAAAGGCTTTATTTGGCCAGGAGCAG 427  
421 GTTTTCATTTTTTGGAGAGCGGAAACATATTAATCTCGAAGCAACAAGCCCGTGATCCCC 480  
428 GTTTTCATTTTTTGGAGAGAGCGGAAACATATTAATCTCGAAGCAACAAGCCCGTGATCCCC 487  
481 CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTTCATGGAATATCAGCCT 540  
488 CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTTCATGGAATATCAGCCT 547  
541 GGAGGGACTTGTGCTCACTTTTGAATAGATATGAGACCAAGTTAGATGAATAAAGCTGATA 600  
548 GGAGGGACTTGTGCTCACTTTTGAATAGATATGAGACCAAGTTAGATGAATAAAGCTGATA 607  
601 CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTCAACAGCGTTTCATCTGATGGGATACGTG 660  
608 CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTCAACAGCGTTTCATCTGATGGGATACGTG 667  
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668 CATCGACATCAGCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 727  
721 GATTTTGGATCTGCGCGGAAATGAATTCAAAAGATGTTGAATGCAAACTCCCGATT 780  
728 GATTTTGGATCTGCGCGGAAATGAATTCAAAAGATGTTGAATGCAAACTCCCGATT 787  
781 GGGACCCAGATTAACATGGCTCTGAAAGTGTGATGTAACCGGGATGGAAGGCAAGGC 840  
788 GGGACCCAGATTAACATGGCTCTGAAAGTGTGATGTAACCGGGATGGAAGGCAAGGC 847  
841 ACCTACCGCTGGACTGTGACTGTGCTGCTGAGTGGCGTGTGCTGATGAGATGATTAT 900  
848 ACCTACCGCTGGACTGTGACTGTGCTGAGTGGCGTGTGCTGATGAGATGATTAT 907  
901 GGGAGATCCCCCTTCGAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTC 960  
908 GGGAGATCCCCCTTCGAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTC 967  
961 CAGCGGTTTTTGAATTTTCAGATGACCCCAAGTGAAGAGTGTGCTTCTGTGATTCGATT 1020  
968 CAGCGGTTTTTGAATTTTCAGATGACCCCAAGTGAAGAGTGTGCTTCTGTGATTCGATT 1027  
1021 CAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCAATCCT 1080  
1028 CAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCAATCCT 1087  
1081 TTCTTCTCTAAATTTGACTGGAACAACATTCGTAACTCTCTCCGCCCTTCGTTCCCAAC 1140  
1088 TTCTTCTCTAAATTTGACTGGAACAACATTCGTAACTCTCTCCGCCCTTCGTTCCCAAC 1147  
1141 CTCAAGTCCGACGATGACCTCCAAATTTTGAATGAACAGAGAAATTCGTGGGTTTCA 1200  
1148 CTCAAGTCCGACGATGACCTCCAAATTTTGAATGAACAGAGAAATTCGTGGGTTTCA 1207  
1201 TCCTCTCCGTCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGACCTGCTTTGTGGGG 1260  
1208 TCCTCTCCGTCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGACCTGCTTTGTGGGG 1267  
1261 TTTTCTGACAGCAGGCACTGGGATTTCTTGATAGATCTCAGTCTGTGTGTGGGTCG 1320  
1268 TTTTCTGACAGCAGGCACTGGGATTTCTTGATAGATCTCAGTCTGTGTGTGGGTCG 1327  
1321 GACTCCCTGCGACGATAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGACTA 1380  
1328 GACTCCCTGCGACGATAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGACTA 1387

QY 1381 CAAGACTCTCAGACAAGTGTCAAGGATATTTATTTCCGACCGGCTCTCTTCCCTTGC 1440  
Db 1388 CAAGACTCTCAGACAAGTGTCAAGGATATTTATTTCCGACCGGCTCTCTTCCCTTGC 1447  
QY 1441 TCAGAGATCTCTCCCGTCCGCTATATGCAAGGGATCCGCGGCGGCTCTGCTGGCTCTGA 1500  
Db 1448 TCAGAGATCTCTCCCGTCCGCTATATGCCAGGGATCCGCGGCGGCTCTGCTGGCTCTGA 1507  
QY 1501 GCCGCTGATCCGTA 1515  
Db 1508 GCCGCTGATCCGTA 1522  
RESULT 5  
ABZ68726  
ID ABZ68726 standard; DNA; 1765 BP.  
XX  
AC ABZ68726;  
XX  
DT 16-MAY-2003 (first entry)  
XX  
Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.  
Db Human; citron rho/rac-interacting kinase-short kinase; obesity;  
KW chronic obstructive pulmonary disease; hypertension; diabetes;  
KW coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;  
KW gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;  
KW polycystic ovarian syndrome; fertility; depression; gene; ss.  
XX  
OS Homo sapiens.  
XX  
Key Location/Qualifiers  
FH CDS l. 1494  
FT /tag= a  
FT /product= "citron rho/rac-interacting kinase-short  
FT kinase"  
XX WO2003004629-A2.  
XX 16-JAN-2003.  
XX 01-JUL-2002; 2002WO-EP007229.  
XX PF  
XX 02-JUL-2001; 2001US-0301853P.  
XX PR 10-DEC-2001; 2001US-0337130P.  
XX PR 25-APR-2002; 2002US-0375015P.  
XX  
XX (FARB ) BAYER AG.  
XX  
XX Zhu Z;  
XX WPI; 2003-221595/21.  
DR P-PSDB; ABP97687.  
XX  
XX New human citron rho/rac-interacting kinase-short kinase polypeptide and  
PT polynucleotide for preventing or treating diseases associated with the  
PT polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary  
PT disease.  
XX  
XX Claim 1; Fig 18; 145pp; English.  
XX  
CC The present sequence encodes a human citron rho/rac-interacting kinase-  
CC short kinase polypeptide. The polynucleotide and polypeptide of the  
CC invention are useful in preventing, ameliorating, or treating diseases  
CC associated with the polypeptide dysfunction. The expression vector or the  
CC reagent is useful in the preparation of a medicament for modulating the  
CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
CC disease, such as obesity or chronic obstructive pulmonary disease. These  
CC may also be used for treating obesity/ overweight-associated  
CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
CC apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced







Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic; hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hiv; neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic; hyperlipidaemia; enzyme; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 55..6219

XX FT /\*tag= a

XX FT /product= "Human kinase (PKIN)-21"

XX WO200233099-A2.

XX 25-APR-2002.

XX 20-OCT-2001; 2001WO-US047728.

XX 20-OCT-2000; 2000US-0242410P.

XX 27-OCT-2000; 2000US-0244068P.

XX 03-NOV-2000; 2000US-0245708P.

XX 09-NOV-2000; 2000US-0247672P.

XX 16-NOV-2000; 2000US-0249565P.

XX 22-NOV-2000; 2000US-0252730P.

XX 01-DEC-2000; 2000US-0250807P.

XX (INCY-) INCYTE GENOMICS INC.

XX Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C; Yao MG, Ramkumar J, Ding L, Fang YF, Hafalia AJA, Nguyen DB; Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG; Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A; Thangavelu K, Khan FA, Ison CH;

XX WPI; 2002-454603/48.

XX P-PSDB; AAE24150.

XX New human kinase polypeptide, for diagnosing, preventing and treating cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders.

XX Claim 5; Page 207-209; 210pp; English.

XX The invention relates human kinases (PKIN) and their corresponding nucleic acid sequences. PKIN and its DNA are useful for diagnosing, treating and preventing cancer, an immune system disorder (e.g., acquired immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma, atherosclerosis, multiple sclerosis, psoriasis), disorders affecting growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis), cardiovascular disorder (e.g., hypertension, myocardial infarction, Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver, Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia, hyperlipidaemia, obesity), and for assessing the effects of exogenous compounds. Anti-PKIN antibody is useful in a diagnostic test for a condition or a disease associated with the expression of PKIN in a biological sample. A composition comprising PKIN or an agonist or antagonist of PKIN is useful for treating a disease or condition associated with decreased or increased expression of functional PKIN. PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, CC and in somatic or germline gene therapy. The present sequence is human PKIN cDNA

XX Sequence 6298 BP; 1772 A; 1595 C; 1720 G; 1221 T; 0 U; 0 Other;

XX Query Match 92.7%; Score 1404.2; DB 6; Length 6298;

XX Best Local Similarity 99.8%; Pred. No. 0;

		Matches	1406;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	1	GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA	60								
DB	49	GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA	108								
QY	61	CCATTTCGCAACCGCGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATG	120								
DB	109	CCATTTCGCAACCGCGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATG	168								
QY	121	ACTCAACAGAGATGCTCTCTTTCCGAGAAAGGATATTAGATGCCCTCTTTGTTCTC	180								
DB	169	ACTCAACAGAGATGCTCTCTTTCCGAGAAAGGATATTAGATGCCCTCTTTGTTCTC	228								
QY	181	TTTGAAGAATGCACTGAGTCACTGATGAAGATTAAAGCAGCTGAGCACTTTGTCGG	240								
DB	229	TTTGAAGAATGCACTGAGTCACTGATGAAGATTAAAGCAGCTGAGCACTTTGTCGG	288								
QY	241	AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTTCCGCAAGAGACTTCGAA	300								
DB	289	AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGCTTTCCGCAAGAGACTTCGAA	348								
QY	301	GTCAAGATCTTTGTAGTTGTGCTCACTTTGCTGAAGTGCAGTGTGAAGAGAAAGCA	360								
DB	349	GTCAAGATCTTTGTAGTTGTGCTCACTTTGCTGAAGTGCAGTGTGAAGAGAAAGCA	408								
QY	361	ACGGGGACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGGCCAGGAGCAG	420								
DB	409	ACGGGGACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGGCCAGGAGCAG	468								
QY	421	GTTCATTTTTTGAGGAAGAGCGGAAACATATTATCTCGAAGCAACAAGCCGTCGATCCCC	480								
DB	469	GTTCATTTTTTGAGGAAGAGCGGAAACATATTATCTCGAAGCAACAAGCCGTCGATCCCC	528								
QY	481	CAATACAGTATGCTTTTTCAGGACAAAATACCTTTATCTGTCATGGAATATCAGCCT	540								
DB	529	CAATACAGTATGCTTTTTCAGGACAAAATACCTTTATCTGTCATGGAATATCAGCCT	588								
QY	541	GGAGGGGACTTGTGTCACCTTTTGAATAGATATGAGGACCAAGTGAATGAACCTGATA	600								
DB	589	GGAGGGGACTTGTGTCACCTTTTGAATAGATATGAGGACCAAGTGAATGAACCTGATA	648								
QY	601	CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTTCAGAGGCTTCATCTGATGGATAGTG	660								
DB	649	CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTTCAGAGGCTTCATCTGATGGATAGTG	708								
QY	661	CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGT	720								
DB	709	CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGT	768								
QY	721	GATTTTGGATCTGCGCGGAAATGAAATTCAAACAGATGGTGAATCCCAACTCCGATTT	780								
DB	769	GATTTTGGATCTGCGCGGAAATGAAATTCAAACAGATGGTGAATCCCAACTCCGATTT	828								
QY	781	GGGACCCAGATTTACATGCTCTCTGAAGTGTGACTGTGATGAACGGGATGGAAGGC	840								
DB	829	GGGACCCAGATTTACATGCTCTCTGAAGTGTGACTGTGATGAACGGGATGGAAGGC	888								
QY	841	ACTACGGCTGAGCTGTGACTGGTGGTCAAGTGGGCGTGAATGCCCTATGAGATGATTAT	900								
DB	889	ACTACGGCTGAGCTGTGACTGGTGGTCAAGTGGGCGTGAATGCCCTATGAGATGATTAT	948								
QY	901	GGGAGATCCCTCTGCGAGAGGAACTCTGCCAGAACCTTCATTAACATTATGAATTC	960								
DB	949	GGGAGATCCCTCTGCGAGAGGAACTCTGCCAGAACCTTCATTAACATTATGAATTC	1008								
QY	961	CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAATTTCTTGATCTGATT	1020								
DB	1009	CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAATTTCTTGATCTGATT	1068								
QY	1021	CAAAGCTTTGTGGCGCCAGAAAGAGACATGAAGTTTGAAGGTTCTTGTCTCCATCCT	1080								
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QY 1081 TTCTTCTCTAAATTTGACTGGAACAACATTCGTAACTCTCTCTCCCTCTCGTTCCACC 1140
Db 1129 TTCTTCTCTAAATTTGACTGGAACAACATTCGTAACTCTCTCTCCCTCTCGTTCCACC 1188
QY 1141 CTCAAGTCGACGATGACGACCTCCAAATTTTGTATGAACACAGAGAAGAAATTCGTGGTTTCA 1200
Db 1189 CTCAAGTCGACGATGACGACCTCCAAATTTTGTATGAACACAGAGAAGAAATTCGTGGTTTCA 1248
QY 1201 TCCTCTCGTCCAGCTGAGCCCTCAGGCTTCCTCGGTTGAAGAACTGCGGTTTGTGGGG 1260
Db 1249 TCCTCTCGTCCAGCTGAGCCCTCAGGCTTCCTCGGTTGAAGAACTGCGGTTTGTGGGG 1308
QY 1261 TTTTTCGTACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1320
Db 1309 TTTTTCGTACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1368
QY 1321 GACTCCCTCGCAAGACTAGCTCCATGGAAGAAATCTTCTCATCAAAAGCAAGAGCTA 1380
Db 1369 GACTCCCTCGCAAGACTAGCTCCATGGAAGAAATCTTCTCATCAAAAGCAAGAGCTA 1428
QY 1381 CAAGACTCTCAGGACAGTGTCAAGGT 1409
Db 1429 CAAGACTCTCAGGACAGTGTCAAGAT 1457

RESULT 8
ADA05643
ID ADA05643 standard; cDNA; 1870 BP.
XX
AC ADA05643;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV1b encoding cDNA SEQ ID NO:3.
XX
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytosolic; norepinephrine; neuroprotective;
KW antiparkinsonian; antilipemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..1870
FT FT /*tag= a
FT FT /product= "NOV1b"
XX
PN W02003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 09-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0343629P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
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PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381042P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383811P.
PR 01-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX (CURA-) CURAGEN CORP.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ott T, Gorman L, Zerkushen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Bergus C, Dippio VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2003-381626/36.
DR P-PSDB; ADA05644.
XX
PS Claim 20; Page 100; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytosolic, norepinephrine, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence encodes a human NOVX protein from
CC the present invention.
XX
SQ Sequence 1870 BP; 505 A; 416 C; 496 G; 453 T; 0 U; 0 Other;
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Query Match 92.3%; Score 1398.2; DB 8; Length 1870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy	67	GCCAAACGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAAACACCCCTTATGACTCAA	126
Db	74	GCCAGCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAAACACCCCTTATGACTCAA	133
Qy	127	CAGCAGATGTCCTCTCTTTTCCGAGAAGGGATATATAGATGCCCTCTTTGTTCTCTTTGAA	186
Db	134	CAGCAGATGTCCTCTCTTTTCCGAGAAGGGATATATAGATGCCCTCTTTGTTCTCTTTGAA	193
Qy	187	GAATGCACTCAGCCTGCTCTGATGAAGATTAAGCACGCTGAGCAACTTTGTCGGGAAGTAT	246
Db	194	GAATGCACTCAGCCTGCTCTGATGAAGATTAAGCACGCTGAGCAACTTTGTCGGGAAGTAT	253
Qy	247	TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAAGTCAGA	306
Db	254	TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAAGGACTTCGAAGTCAGA	313
Qy	307	AGTCTGTGAGTGTGCTGCTTTGCTGGAAGTGCAGGTGGTAAAGAGAGAAGCAACCGGG	366
Db	314	AGTCTGTGAGTGTGCTGCTTTGCTGGAAGTGCAGGTGGTAAAGAGAGAAGCAACCGGG	373
Qy	367	GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTTGGGCCCAGGAGCAGGTTTCA	426
Db	374	GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTTGGGCCCAGGAGCAGGTTTCA	433
Qy	427	TTTTTTGAGGAAGCGGAAACATATTTATCTCGAAGCAACAGCCCGTGGATCCCCCAATTA	486
Db	434	TTTTTTGAGGAAGCGGAAACATATTTATCTCGAAGCAACAGCCCGTGGATCCCCCAATTA	493
Qy	487	CAGTATGCCCTTTCAGGACAAAATCACCTTTATCTGCTCATGGAAATACAGCCTGGAGGG	546
Db	494	CAGTATGCCCTTTCAGGACAAAATCACCTTTATCTGCTCATGGAAATACAGCCTGGAGGG	553
Qy	547	GACTTGTGTCACCTTTTGAAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT	606
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Qy	607	TACCTAGCTGAGCTGATTTTGGCTGTGTTCAACAGCCTTCACTGATGGGATACGTGCATCGA	666
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Qy	667	GACATCAAGCCTGAGACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT	726
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Qy	727	GGATCTCGCGGAAATGAATTCAAAACAAGATGCTGAATGCCAACTCCCGATTTGGGACC	786
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Qy	787	CCAGATTACATGGCTCTCTGAAGTCTGACTGTGTATGAACCGGGGATGAAAAGGCACCTAC	846
Db	794	CCAGATTACATGGCTCTCTGAAGTCTGACTGTGTATGAACCGGGGATGAAAAGGCACCTAC	853
Qy	847	GGCCTGCACTGTGACTGGTGTGACTGGGCGTGATTCCTATGAGATGATTTATGGGAGA	906
Db	854	GGCCTGCACTGTGACTGGTGTGACTGGGCGTGATTCCTATGAGATGATTTATGGGAGA	913
Qy	907	TCCCCCTTCGCAGAGGAAACCTCTGCGCAGAACCTTTCAATAACATTAATGAATTTCCACGGG	966
Db	914	TCCCCCTTCGCAGAGGAAACCTCTGCGCAGAACCTTTCAATAACATTAATGAATTTCCACGGG	973
Qy	967	TTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTCACTTTCTGATCTGATTCAAAGC	1026
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Qy	1027	TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTTCTGCTGCCATCTCTTCTC	1086
Db	1034	TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTTCTGCTGCCATCTCTTCTC	1093

QY	1087	TCTAAATTTGACTGGAAACAATTCGTGTAAC	TCTCTCCCTCCCTTCGTTCCCAACCTCAAG	1144
DB	1094	TCTAAATTTGACTGGAAACAATTCGTGTAAC	TCTCTCCCTCCCTTCGTTCCCAACCTCAAG	1153
QY	1147	TCCGACCATGACACCTCCCAATTTTGATGAAC	CAGAGAAATTCGTGGGTTTCATCCTCT	1206
DB	1154	TCTGACGATGACACCTCCCAATTTTGATGAAC	CAGAGAAATTCGTGGGTTTCATCCTCT	1213
QY	1207	CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGT	CAAGAACTGCGGTTTGTGGGGTTTTTCG	1266
DB	1214	CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGT	CAAGAACTGCGGTTTGTGGGGTTTTTCG	1273
QY	1267	TACAGCAAGGCACATGGGGATCTTTGGTAGAT	CTGAGTCTGTTGTGCGGGTCTGGACTCC	1326
DB	1274	TACAGCAAGGCACATGGGGATCTTTGGTAGAT	CTGAGTCTGTTGTGCGGGTCTGGACTCC	1333
QY	1327	CCTGCCAAGACTAGCTCCATGGAAGAAACTTCT	CATCAAAAGCAAGAGCTTACAAGAC	1386
DB	1334	CCTGCCAAGACTAGCTCCATGGAAGAAACTTCT	CATCAAAAGCAAGAGCTTACAAGAC	1393
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DB	1394	TCTCAGGACAAGTGTCAAAAGT	1416	
RESULT 9				
ABQ78871				
ID	ABQ78871 standard; cDNA; 5877 BP.			
AC	ABQ78871;			
DT	10-OCT-2002 (first entry)			
DE	Human kinase cDNA #2.			
XX	Human; kinase; enzyme; serine-threonine kinase; neotropic; cytosolic;			
KW	Citron rho-interacting kinase; gene therapy; mental disorder; cancer;			
KW	gene; ss.			
XX	Homo sapiens.			
OS	Homo sapiens.			
XX	Key			
FH	CDS			
FT	1. 5877			
FT	/*tag= a			
FT	/product= "Kinase"			
XX	WO200259325-A2.			
XX	01-AUG-2002.			
XX	20-DEC-2001; 2001WO-US050497.			
PF	27-DEC-2000; 2000US-0258335P.			
PR	(LEXI-) LEXICON GENETICS INC.			
XX	Yu X, Miranda M, Friddle CU;			
PI	WPI; 2002-599796/64.			
XX	P-PSDB; ABB81928.			
XX	Novel polynucleotide encoding human proteins that are structurally			
PT	similar to animal kinases, useful for drug screening, diagnosis, in gene			
PT	therapy of disorders and diseases e.g. cancer and pharmacogenomic			
PT	applications.			
XX	Disclosure; Page 44-45; 50pp; English.			
PS	The invention relates to a novel human protein that shares structural			
XX	similarity with animal kinases, including serine-threonine kinases,			
CC	particularly Citron rho-interacting kinases. The proteins of the			
CC	invention have neotropic and cytosolic activity. The polynucleotides may			
CC	have a use in gene therapy. The encoded novel polypeptides are useful for			



PT New human citron rho/rac-interacting kinase (CRIK) polypeptide and  
PT polynucleotide, useful in preventing, ameliorating or treating diseases  
PT associated with human CRIK dysfunction, e.g. obesity, diabetes or  
PT Alzheimer's disease.  
XX  
PS Disclosure; Page 217-222; 237pp; English.  
XX  
CC The invention relates to an isolated polynucleotide encoding a human  
CC citron rho/rac-interacting kinase polypeptide. The isolated  
CC polynucleotide comprises a 6165 or 8603 base pair sequence, given in the  
CC specification. The human citron rho/rac-interacting kinase (CRIK)  
CC polypeptide and polynucleotide are useful in preventing, ameliorating, or  
CC treating diseases associated with human CRIK dysfunction such as obesity  
CC and obesity-associated comorbidities (e.g. hypertension, coronary artery  
CC disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of  
CC cancer including endometrial, breast, prostate and colon cancer),  
CC anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood  
CC disorders, anxiety disorders, Parkinson's disease or Alzheimer's  
CC disease), chronic obstructive pulmonary disease, or diabetes. These can  
CC also be used to treat pain associated with the disorders. The human CRIK  
CC polypeptide is also useful in diagnostic assays or in genetic testing.  
CC The expression vector or the reagent is useful in preparing a medicament  
CC for modulating the activity of a human CRIK in a disease, e.g. obesity, a  
CC central nervous system disorder, or chronic obstructive pulmonary  
CC disease. The fusion protein is useful for generating antibodies against a  
CC CRIK polypeptide and for use in various assay systems. The methods are  
CC useful in producing and detecting the polynucleotide and polypeptide and  
CC in screening for agents that modulate the activity of the human CRIK  
CC polypeptide. This polynucleotide sequence represents a DNA sequence  
CC relating to the human CRIK protein of the invention  
XX  
SQ Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;

Query Match 92.3%; Score 1398.2; DB 9; Length 6156;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 7 ATGCTGAAGTTCAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATT 66  
DB 1 AUGTTGAGTTCAAAATATGAGCGCGGAATCCCTTTGGATGCTGCTGCTGAACCCATT 60  
QY 67 GCCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATGACTCAA 126  
DB 61 GCCAGCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATGACTCAA 120  
QY 127 CAGCAGATGCTCTCTTTCCGAGAGGATATAGATGCCCTCTTTGTTCTTTTGAA 186  
DB 121 CAGCAGATGCTCTCTTTCCGAGAGGATATAGATGCCCTCTTTGTTCTTTTGAA 180  
QY 187 GAATGCAGTCAGCTGCTCTGATGAAGATTAAAGCAGTGAAGCACTTTGTCGGGAAGTAT 246  
DB 181 GAATGCAGTCAGCTGCTCTGATGAAGATTAAAGCAGTGAAGCACTTTGTCGGGAAGTAT 240  
QY 247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTTCCGCAAGGACTTCGAAAGTCAGA 306  
DB 241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTTCCGCAAGGACTTCGAAAGTCAGA 300  
QY 307 AGTCTTTGATGTTGTTGCTACTTTGCTGAAAGTGAAGTGAAGAGAAAGCAACCGGG 366  
DB 301 AGTCTTTGATGTTGTTGCTACTTTGCTGAAAGTGAAGTGAAGAGAAAGCAACCGGG 360  
QY 367 GACATCTATGCTATGAAGTGATGAAGAGGCTTTATTTGGCCAGGAGCAGGTTTCA 426  
DB 361 GACATCTATGCTATGAAGTGATGAAGAGGCTTTATTTGGCCAGGAGCAGGTTTCA 420  
QY 427 TTTTGTGAGGAGAGCGGAACATATTATCTCGAAGCACAAAGCCGCTGGATCCGCCAATTA 486  
DB 421 TTTTGTGAGGAGAGCGGAACATATTATCTCGAAGCACAAAGCCGCTGGATCCGCCAATTA 480  
QY 487 CAGTATGCCCTTTCAGGACAAAATATCACTTTTATCTGGTCAATGAATATCAGCTTGAGGG 546  
DB 481 CAGTATGCCCTTTCAGGACAAAATATCACTTTTATCTGGTCAATGAATATCAGCTTGAGGG 540

## RESULT 11

ABQ78870  
ID ABQ78870 standard; cDNA; 6165 BP.  
XX  
AC ABQ78870;  
XX AC  
DT 10-OCT-2002 (first entry)  
XX  
DE Human kinase cDNA #1.  
XX  
KW Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;  
KW Citron rho-interacting kinase; gene therapy; mental disorder; cancer;

QY 547 GACTTCTGCTCACTTTTGAATAGATAGAGGACCACTTAGATGAAACCTGATACAGTTT 606  
DB 541 GACTTCTGCTCACTTTTGAATAGATAGAGGACCACTTAGATGAAACCTGATACAGTTT 600  
QY 607 TACCTAGCTGAGCTGATTTTGGCTGTTTACAGGGTTTCATCTGATGGATACGTCATCGA 666  
DB 601 TACCTAGCTGAGCTGATTTTGGCTGTTTACAGGGTTTCATCTGATGGATACGTCATCGA 660  
QY 667 GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726  
DB 661 GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 720  
QY 727 GATCTGCCCGGAAATGAATTCAAACAGATGGTGAATGCCAACTCCGATTTGGAC 786  
DB 721 GATCTGCCCGGAAATGAATTCAAACAGATGGTGAATGCCAACTCCGATTTGGAC 780  
QY 787 CCAGATTATCATGGCTCTCAAGTGTGCTGATGAACGGGATGGAAGGACCACTAC 846  
DB 781 CCAGATTATCATGGCTCTCAAGTGTGCTGATGAACGGGATGGAAGGACCACTAC 840  
QY 847 GGCCTGGAATGTGACTGGTGGTCAAGTGGGCGTGAATTCCTATCAGATGATTTATGGAGA 906  
DB 841 GGCCTGGAATGTGACTGGTGGTCAAGTGGGCGTGAATTCCTATCAGATGATTTATGGAGA 900  
QY 907 TCCCTCTTCGAGAGGAACTCTGCGCAACCTTCAATAACATTAATGAATTTCCAGCG 966  
DB 901 TCCCTCTTCGAGAGGAACTCTGCGCAACCTTCAATAACATTAATGAATTTCCAGCG 960  
QY 967 TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTACTTCTTGTATCTGATCAAGC 1026  
DB 961 TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTACTTCTTGTATCTGATCAAGC 1020  
QY 1027 TTGTTGTCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTTTCTTC 1086  
DB 1021 TTGTTGTCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCTTTCTTC 1080  
QY 1087 TCTAAATTTGACTGGAAACCAACTTCCTCTCCCTCCCTTCGTTCCCACTCAAG 1146  
DB 1081 TCTAAATTTGACTGGAAACCAACTTCCTCTCCCTCCCTTCGTTCCCACTCAAG 1140  
QY 1147 TCCGAGATGACACTTCCAAATTTTGAATGAACAGAGAGAAATTCGTTGGGTTTCATCTCT 1206  
DB 1141 TCTGAGATGACACTTCCAAATTTTGAATGAACAGAGAGAAATTCGTTGGGTTTCATCTCT 1200  
QY 1207 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGACTGCGCTTTGTTGGGTTTCG 1266  
DB 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGACTGCGCTTTGTTGGGTTTCG 1260  
QY 1267 TACAGCAAGGCACTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTCGGGCTCGGACTCC 1326  
DB 1261 TACAGCAAGGCACTGGGGATTTCTTGGTAGATCTGAGTCTGTTGTCGGGCTCGGACTCC 1320  
QY 1327 CTGCGCAAGCTAGCTTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTACAAGAC 1386  
DB 1321 CTGCGCAAGCTAGCTTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTACAAGAC 1380  
QY 1387 TCTCAGGCAAGTGTCCCAAGT 1409  
DB 1381 TCTCAGGCAAGTGTCCCAAGT 1403







Qy 1387 TCTCAGGACAAGTGTCAAGGT 1409  
 Db 1381 TCTCAGGACAAGTGTCAAGAT 1403

## RESULT 12

AAU55214  
 ID AAL55214 standard; DNA; 6165 BP.

XX AAL55214;

XX 01-MAY-2003 (first entry)

XX Human CR1K encoding DNA sequence, SEQ ID No 1.

XX Anorectic; hypotensive; cardiac; antilipemic; cerebroprotective;  
 KW antieut; osteopathic; antiarthritic; cytosolic; antidepressant;  
 KW immunomodulator; antinflammatory; antidiabetic; analgesic;  
 KW human citron rho/rac-interacting kinase; enzyme; CR1K; ameliorating;  
 KW obesity; comorbidities; cancer; anorexia; cachexia; bulimia;  
 KW central nervous system disorder; chronic obstructive pulmonary disease;  
 KW diabetes; pain; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..6165

XX FT /\*tag= a  
 FT /product= "Human CR1K protein"

XX PN W02003004523-A1.

XX PD 16-JAN-2003.

XX PF 28-JUN-2002; 2002WO-EP007156.

XX PR 02-JUL-2001; 2001US-0301841P.

XX PR 11-DEC-2001; 2001US-0338651P.

XX PR 25-APR-2002; 2002US-0375014P.

XX PA (FARB ) BAYER AG.

XX PI Zhu Z;

XX WPI: 2003-221576/21.

XX DR P-PSDB; AAO26959.

XX New human citron rho/rac-interacting kinase (CR1K) polypeptide and  
 PT polynucleotide, useful in preventing, ameliorating or treating diseases  
 PT associated with human CR1K dysfunction, e.g. obesity, diabetes or  
 PT Alzheimer's disease.

XX Example 1; Fig 1; 237pp; English.

XX The invention relates to an isolated polynucleotide encoding a human  
 CC citron rho/rac-interacting kinase polypeptide. The isolated  
 CC polynucleotide comprises a 6165 or 8603 base pair sequence, given in the  
 CC specification. The human citron rho/rac-interacting kinase (CR1K)  
 CC polypeptide and polynucleotide are useful in preventing, ameliorating, or  
 CC treating diseases associated with human CR1K dysfunction such as obesity  
 CC and obesity-associated comorbidities (e.g. hypertension, coronary artery  
 CC disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of  
 CC cancer including endometrial, breast, prostate and colon cancer),  
 CC anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood  
 CC disorders, anxiety disorders, Parkinson's disease or Alzheimer's  
 CC disease), chronic obstructive pulmonary disease, or diabetes. These can  
 CC also be used to treat pain associated with the disorders. The human CR1K  
 CC polypeptide is also useful in diagnostic assays or in genetic testing.  
 CC The expression vector or the reagent is useful in preparing a medicament  
 CC for modulating the activity of a human CR1K in a disease, e.g. obesity, a  
 CC central nervous system disorder, or chronic obstructive pulmonary  
 CC disease. The fusion protein is useful for generating antibodies against a

CC CR1K polypeptide and for use in various assay systems. The methods are  
 CC useful in producing and detecting the polynucleotide and polypeptide and  
 CC in screening for agents that modulate the activity of the human CR1K  
 CC polypeptide. This polynucleotide sequence represents a DNA sequence  
 CC encoding a human CR1K protein of the invention

XX  
 SQ Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;

Query Match 92.3%; Score 1398.2; DB 9; Length 6165;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 ATGTTGAAGTTCAAATATGAGCGCGGAATCTTTGGATGCTGCTGCTGAACCCATT 66  
 Db 1 ATGTTGAAGTTCAAATATGAGCGCGGAATCTTTGGATGCTGCTGCTGAACCCATT 60  
 Qy 67 GCCAACCGGGCTCCAGGCTGAATCTGTTCCAGGGGAAACACCCCTTTATGACTCAA 126  
 Db 61 GCCAGCGGGCTCCAGGCTGAATCTGTTCCAGGGGAAACACCCCTTTATGACTCAA 120  
 Qy 127 CAGCAGATGCTCCTCTTTCCGAGGAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186  
 Db 121 CAGCAGATGCTCCTCTTTCCGAGGAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180  
 Qy 187 GAATGCAGTCAGCTGCTCTGATGAAGATTAAGCACGTCAGCAACTTTTGTCCGGAAGTAT 246  
 Db 181 GAATGCAGTCAGCTGCTCTGATGAAGATTAAGCACGTCAGCAACTTTTGTCCGGAAGTAT 240  
 Qy 247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAGACATTCGAAAGTCAGA 306  
 Db 241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAGACATTCGAAAGTCAGA 300  
 Qy 307 AGTCTTTGATAGTTGCTGCTCACTTTGCTGAAGTCAGTGTAGAGAGAAAGCAACCGGG 366  
 Db 301 AGTCTTTGATAGTTGCTGCTCACTTTGCTGAAGTCAGTGTAGAGAGAAAGCAACCGGG 360  
 Qy 367 GACATCTATGCTATGAAAGTGTATGAAGAAGAGGCTTTATTTGCCCCAGGACGAGTTTCA 426  
 Db 361 GACATCTATGCTATGAAAGTGTATGAAGAAGAGGCTTTATTTGCCCCAGGACGAGTTTCA 420  
 Qy 427 TTTTGTGAGGAAGAGCGGAAACATATTATCTCGAAGCACAAAGCCCTGGATCCCCCAATTA 486  
 Db 421 TTTTGTGAGGAAGAGCGGAAACATATTATCTCGAAGCACAAAGCCCTGGATCCCCCAATTA 480  
 Qy 487 CAGTATGCTTTTCAGGACAAATACCTTTATCTGCTCATGGAATATCAGCCTCGAGGG 546  
 Db 481 CAGTATGCTTTTCAGGACAAATACCTTTATCTGCTCATGGAATATCAGCCTCGAGGG 540  
 Qy 547 GACTTGTCTCACTTTTGAATAGATATGAGGACCACTTAGATGAAACCTGTATACAGTTT 606  
 Db 541 GACTTGTCTCACTTTTGAATAGATATGAGGACCACTTAGATGAAACCTGTATACAGTTT 600  
 Qy 607 TACCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGATACGTGCATCGA 666  
 Db 601 TACCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGATACGTGCATCGA 660  
 Qy 667 GACATCAAGCTGAGCAACATTTCTGTTGACCCGACAGGACACATCAAGCTGGTGGATTTT 726  
 Db 661 GACATCAAGCTGAGCAACATTTCTGTTGACCCGACAGGACACATCAAGCTGGTGGATTTT 720  
 Qy 727 GGATCTGCCCGCAAAATGAATTAATCAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 786  
 Db 721 GGATCTGCCCGCAAAATGAATTAATCAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780  
 Qy 787 CCAGATTATCATGGCTCCTGAAGTGTGATGATGAACCGGGATGGAAAGGACACCTAC 846  
 Db 781 CCAGATTATCATGGCTCCTGAAGTGTGATGATGAACCGGGATGGAAAGGACACCTAC 840  
 Qy 847 GGCCTTGACTGTGACTGGTGGTTCAGTGGCGGTGATTCCTATGAGATGATTTATGGGAGA 906  
 Db 841 GGCCTTGACTGTGACTGGTGGTTCAGTGGCGGTGATTCCTATGAGATGATTTATGGGAGA 900  
 Qy 907 TCCCCCTTCGAGAGGGGAACCTCTGCCAGAACCTTCAATAACATTATTAATTTCCAGCGG 966



QY 547 GACTGCTGCTCACTTTTGAATAGATATGAGACAGATTAGATGAATAACCTGATACAGTTT 606  
Db 541 GACTGCTGCTCACTTTTGAATAGATATGAGACAGATTAGATGAATAACCTGATACAGTTT 600  
QY 607 TACTAGCTGAGCTGATTTTGGCTGTTTCAACAGCTTTCATCTGATGGATACGTCGATCGA 666  
Db 601 TACTAGCTGAGCTGATTTTGGCTGTTTCAACAGCTTTCATCTGATGGATACGTCGATCGA 660  
QY 667 GACATCAAGCCTGAGAAATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726  
Db 661 GACATCAAGCCTGAGAAATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 720  
QY 727 GGATCTCCCGGAAATGAATTAACAAGATGGTGAATGCCAAAATCTCCGATTTGGAC 786  
Db 721 GGATCTCCCGGAAATGAATTAACAAGATGGTGAATGCCAAAATCTCCGATTTGGAC 780  
QY 787 CCAGATTACATGCTCTGAGAGTCTGACTGATGAACGGGATGGAAGAAGCACCTAC 846  
Db 781 CCAGATTACATGCTCTGAGAGTCTGACTGATGAACGGGATGGAAGAAGCACCTAC 840  
QY 847 GGCTTGACTGTGACTGGTGGTCACTGGGCTGATTCCTATGAGATGATTTATGGGAGA 906  
Db 841 GGCTTGACTGTGACTGGTGGTCACTGGGCTGATTCCTATGAGATGATTTATGGGAGA 900  
QY 907 TCCCTTTCGAGAGGAACTCTGCCAGAACCTTCAATTAACATTAATTAATTTCCAGCGG 966  
Db 901 TCCCTTTCGAGAGGAACTCTGCCAGAACCTTCAATTAACATTAATTAATTTCCAGCGG 960  
QY 967 TTTTGGAAATTCAGATGACCCCAAGTGAAGTCACTTTCTTGATCTGATTCGAAGC 1026  
Db 961 TTTTGGAAATTCAGATGACCCCAAGTGAAGTCACTTTCTTGATCTGATTCGAAGC 1020  
QY 1027 TTGTTGCGCCAGAGAGAGACTGAAGTGTGAAGTCTTTGCTGCCATCTTTCTTC 1086  
Db 1021 TTGTTGCGCCAGAGAGAGACTGAAGTGTGAAGTCTTTGCTGCCATCTTTCTTC 1080  
QY 1087 TCTAAATTCAGTGGAAACAATTCGTAATCTCTCCCTCCCTTCGTTCCACCTCAAG 1146  
Db 1081 TCTAAATTCAGTGGAAACAATTCGTAATCTCTCCCTCCCTTCGTTCCACCTCAAG 1140  
QY 1147 TCCGAGATGACACTCCATTTTGTATGAACAGAGAGAAATTCGTTGGTTTCACTCT 1206  
Db 1141 TCTGAGATGACACTCCATTTTGTATGAACAGAGAGAAATTCGTTGGTTTCACTCT 1200  
QY 1207 CCGTGCCAGCTGAGCCCTCAGGCTCTTCGGGTGAAGAACTCGCTTTGTTGGGTTTCG 1266  
Db 1201 CCGTGCCAGCTGAGCCCTCAGGCTCTTCGGGTGAAGAACTCGCTTTGTTGGGTTTCG 1260  
QY 1267 TACAGCAAGCAGCTGGGGATTTCTTGTGATCTGAGTCTGTTGTGCTGGGTCTGGACTCC 1326  
Db 1261 TACAGCAAGCAGCTGGGGATTTCTTGTGATCTGAGTCTGTTGTGCTGGGTCTGGACTCC 1320  
QY 1327 CTGCGCAAGCTAGCTCCATGGAAGAAATCTTCAATCAAAAGCAAGAGCTTACAAGC 1386  
Db 1321 CTGCGCAAGCTAGCTCCATGGAAGAAATCTTCAATCAAAAGCAAGAGCTTACAAGC 1380  
QY 1387 TCTCAGCAAGCTGTCACAGGT 1409  
Db 1381 TCTCAGCAAGCTGTCACAGAT 1403

RESULT 14  
AAD39191  
ID AAD39191 standard; cdna; 6574 BP.  
XX  
AC AAD39191;  
DT  
XX 04-OCT-2002 (first entry)  
XX Human MDPK cDNA.  
DE  
XX Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein;  
KW tumorigenesis; tumour growth; tumour metastasis; viral infection;  
KW

KW skeletal muscle disorder; muscular dystrophy; myotonic dystrophy;  
KW immune disorder; neoplastic disorder; gene therapy; gene; ss.  
OS Homo sapiens.  
PH Key Location/Qualifiers  
FT 5'UTR 1..18  
FT CDS /\*tag= a  
FT /\*tag= b  
FT /\*tag= c  
FT misc\_feature 19..6177  
FT /\*tag= d  
FT 3'UTR 6181..6574  
XX WO200234896-A2.  
XX 02-MAY-2002.  
XX 23-OCT-2001; 2001WO-US050636.  
XX 23-OCT-2000; 2000US-0242429P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Kapeller-Libermann R;  
XX WPI; 2002-479720/51.  
XX P-PSDB; AAE24079.  
XX Human myotonic dystrophy type protein kinase polypeptide and  
XX polynucleotide useful for prognosticating, diagnosing, preventing or  
XX inhibiting tumorigenesis, tumor growth, tumor metastasis and viral  
XX infection.  
XX Claim 1; Fig 1; 148pp; English.  
XX The invention relates to human myotonic dystrophy type protein kinase  
XX (MDPK) polypeptides designated as 13245 and nucleic acid molecules  
XX encoding such polypeptides. 13245 molecules are used to develop  
XX diagnostic and therapeutic agents for prognosticating, diagnosing,  
XX preventing, inhibiting, alleviating or curing MDPK-related disorders.  
XX Polypeptides of the invention are used to develop diagnostic and  
XX therapeutic agents for 13245-mediated or related disorders such as  
XX tumorigenesis, tumour growth, tumour metastasis, viral infection of a  
XX cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies),  
XX immune disorders and neoplastic disorders. The invention is also used in  
XX gene therapy. The present sequence is human MDPK cDNA  
SQ Sequence 6574 BP; 1877 A; 1611 C; 1776 G; 1310 T; 0 U; 0 Other;  
Query Match 92.3%; Score 1397.8; DB 6; Length 6574;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGAA 60  
Db 13 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGTGCTGAA 72  
QY 61 CCATTTGCCAACCGGGCTCCAGGCTGAATCTCTTCCAGGGGAAACACCCCTTATG 120  
Db 73 CCATTTGCCAGCGGGCTCCAGGCTGAATCTCTTCCAGGGGAAACACCCCTTATG 132  
QY 121 ACTCAACAGCAGATGCTCTCTCTTTCCAGAGAGGATATTAGATGCCCTCTTTGTTCTC 180  
Db 133 ACTCAACAGCAGATGCTCTCTCTTTCCAGAGAGGATATTAGATGCCCTCTTTGTTCTC 192  
QY 181 TTTGAAGAATGCACTGAGCTGCTCTGATGAAGATTAAGCACTGAGCAACTTTGTCGG 240  
Db 193 TTTGAAGAATGCACTGAGCTGCTCTGATGAAGATTAAGCACTGAGCAACTTTGTCGG 252

Qy	241	AAGTATTCCGACACCATAGCTGAGTTACGGAGCTCCAGCGCTTCGCGCAAAAGGACTTCGAA	300
Dd	253	AAGTATTCCGACACCATAGCTGAGTTACGGAGCTCCAGCGCTTCGCGCAAAAGGACTTCGAA	312
Qy	301	GTCAGAAGTCTTGTAAGTGTGTGTCACCTTTGTCGAAGTGCAGGTGGTAAAGAGAAGAACA	360
Dd	313	GTCAGAAGTCTTGTAAGTGTGTGTCACCTTTGTCGAAGTGCAGGTGGTAAAGAGAAGAACA	372
Qy	361	ACGGGGACATCATGCTATGAAAGTGAATGAAGAAGAGGCTTTATTGGCCCCCAGGAGCAG	420
Dd	373	ACGGGGACATCATGCTATGAAAGTGAATGAAGAAGAGGCTTTATTGGCCCCCAGGAGCAG	432
Qy	421	GTTTTCAATTTTTTAGGAAGACGGGAAACATATTTATCTCGAAGCACAAAGCCCGTGGATCCCC	480
Dd	433	GTTTTCAATTTTTTAGGAAGACGGGAAACATATTTATCTCGAAGCACAAAGCCCGTGGATCCCC	492
Qy	481	CAATTAAGTATGCTTTTCAGGACAAAATAACCTTTTATCTGTCATCGGAATATACAGCCT	540
Dd	493	CAATTAAGTATGCTTTTCAGGACAAAATAACCTTTTATCTGTCATCGGAATATACAGCCT	552
Qy	541	GGAGGGACATTGCTGCACATTTTGAATAGATATGAGGACCAGTTAGATGAAACCTTGATA	600
Dd	553	GGAGGGACATTGCTGCACATTTTGAATAGATATGAGGACCAGTTAGATGAAACCTTGATA	612
Qy	601	CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCACTGATGGGATACGTG	660
Dd	613	CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCACTGATGGGATACGTG	672
Qy	661	CATCGAGACATCAAGCCTGAGAACATTTCTCGTTGACCGCACAGGACACATCAAGCTGGTG	720
Dd	673	CATCGAGACATCAAGCCTGAGAACATTTCTCGTTGACCGCACAGGACACATCAAGCTGGTG	732
Qy	721	GAATTTTGGATCTGCCGCGAAAAATGAAATTCAAAACAAGATGGTGAATGCCAAATCCCAGATT	780
Dd	733	GAATTTTGGATCTGCCGCGAAAAATGAAATTCAAAACAAGATGGTGAATGCCAAATCCCAGATT	792
Qy	781	GGGACCCAGATTACATGGCTCTCGAAGTGCTGATCTGTGATGAACGGGGATGGAAGAAGCC	840
Dd	793	GGGACCCAGATTACATGGCTCTCGAAGTGCTGATCTGTGATGAACGGGGATGGAAGAAGCC	852
Qy	841	ACCTACGGCCTGGACTGTGACTGGTGTGCTAGTGGGCGTGATGCGCTATGAGATGATTTAT	900
Dd	853	ACCTACGGCCTGGACTGTGACTGGTGTGCTAGTGGGCGTGATGCGCTATGAGATGATTTAT	912
Qy	901	GGGAGATCCCCCTTCGCAGAGGGAACTCTGCCAGAACCTTCAATAACATTTAGAAATTC	960
Dd	913	GGGAGATCCCCCTTCGCAGAGGGAACTCTGCCAGAACCTTCAATAACATTTAGAAATTC	972
Qy	961	CAGCGGTTTTGAAATTTCCAGATGACCCCAAAGTAGAGTGACTTTCTTGATCTGATTT	1020
Dd	973	CAGCGGTTTTGAAATTTCCAGATGACCCCAAAGTAGAGTGACTTTCTTGATCTGATTT	1032
Qy	1021	CAAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTTCTGCTGCCATCCCT	1080
Dd	1033	CAAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTTCTGCTGCCATCCCT	1092
Qy	1081	TTCTTCTCTAAAATTTGACTGSAACAAATTCGTAACCTCTCTCCCCCTTCGTTCCCAACC	1140
Dd	1093	TTCTTCTCTAAAATTTGACTGSAACAAATTCGTAACCTCTCTCCCCCTTCGTTCCCAACC	1152
Qy	1141	CTCAAGTCCGACGATGACACCTCCAATTTTGATGAACAGAGAAGAATTCGTGGGTTTCA	1200
Dd	1153	CTCAAGTCTGACGATGACACCTCCAATTTTGATGAACAGAGAAGAATTCGTGGGTTTCA	1212
Qy	1201	TCCTCTCCGTCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGCTTTGTGGGG	1260
Dd	1213	TCCTCTCCGTCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGCTTTGTGGGG	1272
Qy	1261	TTTTTCGTAACAGCAAGGCACTGGGGAATCTTGGTAGATCTGAGTCTGTGTGTCGGGCTG	1320
Dd	1273	TTTTTCGTAACAGCAAGGCACTGGGGAATCTTGGTAGATCTGAGTCTGTGTGTCGGGCTG	1332

Qy	1321	GACTCCCTGCCAAGACTAGTCCATGGAAAAAAGAACTTCTCATCAAAAAGCAAGAGCTA	1380
Db	1333	GACTCCCTGCCAAGACTAGTCCATGGAAAAAAGAACTTCTCATCAAAAAGCAAGAGCTA	1392
Qy	1381	CARAGCTCTCAGCACAAGTGTCAACAAGGT	1409
Db	1393	CARAGCTCTCAGCACAAGTGTCAACAAGT	1421
RESULT 15			
ADF60992			
ID	ADF60992 standard; DNA; 6574 BP.		
XX			
AC	ADF60992;		
XX			
DT	12-FEB-2004 (first entry)		
XX			
DE	Pain associated human 2207 gene.		
XX			
KW	Pain modulation; pain disorder; painful disorder; potassium channel;		
KW	kinase expression; inflammatory pain; chronic pain; neuropathic pain;		
KW	causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain;		
KW	analgesic; antiinflammatory; gene; ds.		
XX			
OS	Homo sapiens.		
XX			
FN	US2003153525-A1.		
XX			
PD	14-AUG-2003.		
XX			
PF	19-DEC-2002; 2002US-00325430.		
XX			
PR	19-DEC-2001; 2001US-0341953P.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Silos-Santiago I, Rosenfeld JB;		
DR			
XX	WPI; 2003-897732/82.		
DR	P-PSDB; ADF60994.		
XX			
PT	Identifying a compound capable of treating a pain disorder comprises		
PT	assessing the ability of the compound to modulate specific, e.g., kinases		
PT	or potassium channel, nucleic acid expression or polypeptide activities.		
XX			
PS	Disclosure; SEQ ID NO 10; 80pp; English.		
XX			
CC	The present invention relates to a method for identifying a compound		
CC	capable of modulating pain or painful disorders. The method comprises		
CC	assaying the ability of the compound to modulate specific nucleic acid		
CC	expression or polypeptide activity e.g. potassium channel, or kinase		
CC	expression/activity. The method and compounds are useful for treating		
CC	pain or painful disorders e.g. inflammatory pain, chronic pain,		
CC	neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache		
CC	pain and tissue pain. The present sequence encodes a human protein		
CC	associated with pain.		
XX			
SQ	Sequence 6574 BP; 1877 A; 1611 C; 1776 G; 1310 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity 92.3%; Score 1397.8; DB 10; Length 6574;			
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
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Qy	61	CCCATTCGCAACCGGGCTCCAGCTCAATCTGTCTTCTCCAGGGAAACCAACCCCTTATG	120
Db	73	CCCATTCGCAACCGGGCTCCAGCTCAATCTGTCTTCTCCAGGGAAACCAACCCCTTATG	132
Qy	121	ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGGATATAGATGCCCTCTTTGTTCTC	180

Db 133 ACTCAACAGCAGATGTCTCTCTTTCCGAGAAAGGATATTAGATGCCCTCTTTTGTTC 192  
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Search completed: March 19, 2005, 08:21:29  
Job time : 774.108 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 06:53:57 ; Search time 6455.94 Seconds  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sbs.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1515	100.0	1515	6 AR253937	AR253937 Sequence
2	1515	100.0	1515	6 AR453415	AR453415 Sequence
3	1510.2	99.7	2066	6 AX642956	AX642956 Sequence
4	1505.8	99.4	1785	6 AX671044	AX671044 Sequence
5	1481.8	97.8	1485	6 AX671037	AX671037 Sequence
6	1404.2	92.7	6298	6 AX504254	AX504254 Sequence
7	1404.2	92.7	8576	9 AY257469	AY257469 Homo sapi
8	1399.4	92.4	1799	9 AY209000	AY209000 Homo sapi
9	1398.2	92.3	5877	6 AR534559	AR534559 Sequence
10	1398.2	92.3	5877	6 AX574427	AX574427 Sequence
11	1398.2	92.3	6156	6 AX671112	AX671112 Sequence
12	1398.2	92.3	6165	6 AR534558	AR534558 Sequence
13	1398.2	92.3	6165	6 AX574425	AX574425 Sequence
14	1398.2	92.3	6165	6 AX671105	AX671105 Sequence
15	1398.2	92.3	8603	6 AX671108	AX671108 Sequence
16	1397.8	92.3	6574	6 AX429512	AX429512 Sequence
17	1391.8	91.9	6159	6 AX429514	AX429514 Sequence
18	1382	91.2	6159	6 AX166510	AX166510 Sequence
19	1375.8	90.8	6189	6 AX503780	AX503780 Sequence

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26	760.8	50.2	1133	6 AR411948	AR411948 Sequence
27	760.8	50.2	1133	6 AR475453	AR475453 Sequence
28	578.8	38.2	2896	6 CQ498283	CQ498283 Sequence
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ALIGNMENTS

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LOCUS AR253937 1515 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 1 from patent US 6479269.  
ACCESSION AR253937  
VERSION AR253937.1 GI:27302420  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1515)  
AUTHORS Webster M., Yan, C., Di Francesco, V. and Beasley, E.M.  
TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof  
JOURNAL Patent: US 6479269-A 1 12-NOV-2002;  
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source Location/Qualifiers  
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Qy	1441	TC	CAGGATCTCCCGTCCGTATATGTCACAGGATTCGCCCCGGGGCGCTGCTGGCTCTGA	1500
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DEFINITION	Sequence 1 from patent US 6680188.			
ACCESSION	AR453415			
VERSION	AR453415.1		GI:42686143	
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1515)			
AUTHORS	Webster, M., Yan, C., Di Francesco, V. and Beasley, B.M.			
TITLE	Isolated human kinase proteins, nucleic acid molecules encoding			
JOURNAL	human kinase proteins, and uses thereof			
FEATURES	Patent: US 6680188-A 1 20-JAN-2004;			
source	Location/Qualifiers			
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Best Local Similarity	100.0%; Pred. NO. 0;			
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AX642956  
LOCUS  
DEFINITION  
Sequence 33 from Patent WO01096547.  
ACCESSION  
AX642956  
VERSION  
AX642956.1 GI:28550096  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1  
AUTHORS  
Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,  
Gandhi,A.R., Tribouley,C.M., Walia,N., Igo,M.G., Lu,D.A.,  
Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,  
Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,  
Hafalia,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,  
Recipon,S.A., Azimzai,Y., Policky,J.L., Ding,L., Grether,M.,  
Elliot,V.S., Thangavelu,K., Batra,S. and Ison,C.H.  
HUMAN KINASES  
Patent: WO 01096547-A 33 20-DEC-2001;  
Incyte Genomics, Inc. (US)  
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LOCUS 1485 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 1 from Patent WO03004629.  
ACCESSION AX671037  
VERSION AX671037.1 GI:29329507  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Zhu, Z.  
TITLE Regulation of human citron rho/rac-interacting kinase-short kinase  
JOURNAL Patent: WO 03004629-A 1 16-JAN-2003;  
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RESULT 7
AY257469
LOCUS AY257469 8576 bp mRNA linear PRI 23-APR-2003
DEFINITION Homo sapiens rho/rac-interacting citron kinase (CIT) mRNA, complete cds.
ACCESSION AY257469
VERSION AY257469.1 GI:30088969
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 8576)
Huang, C.O., Wu, S.L., Shan, Y.X., Liu, S. and Xiao, P.J.
Direct Submission
Submitted (18-MAR-2003) Department of Biochemistry and Molecular
Biology, Basic Medicine, Suzhou University, Renming Road 48,
Suzhou, Jiangsu 215007, China
Location/Qualifiers
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## ORIGIN

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Query Match 92.7%; Score 1404.2; DB 9; Length 8576;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1406; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DEFINITION
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ACCESSION
    AY209000
VERSION
    AY209000.1 GI:37784566
KEYWORDS
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SOURCE
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    Mao, Y., Xie, Y. and Wu, Q.
    Cloning and characterizing a novel human CRIK-SK gene
    Unpublished
REFERENCE
    2 (bases 1 to 1799)
    Mao, Y., Xie, Y. and Wu, Q.
    Direct Submission
    Submitted (02-JAN-2003) Institute of Genetics, Fudan University,
    220 Handan Road, Shanghai 200433, P.R. China
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AUTHORS			
Yu, X.S., Miranda, M. and Friddle, C.J.			
TITLE			
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LOCUS Sequence 3 from Patent WO02059325.
DEFINITION AX574427
ACCESSION AX574427
VERSION AX574427.1 GI:27551752
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Yu, X., Miranda M. and Fridele, C.J.
AUTHORS Human kinases and polynucleotides encoding the same
TITLE Patent: WO 02059325-A 3 01-AUG-2002;
JOURNAL Lexicon Genetics Incorporated (US)
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Db 301 AGTCTTGTAGGTTGTGTTCACTTTTGTCTCAAGTGCAGGTGGTGAAGAGAAAGCAACCGGG 360
QY 367 GACATCTATGCTATGAAGTGAATGAAGAGGCTTTATGGCCCGAGGACGAGTTTCA 426
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Db 481 CAGTATGCTTTTTCAGGACAAAAATCACCTTTATCTGGTCAATGGAATATCAGCTTGAGGG 540
QY 547 GACTTGTCTGCTCACTTTTGAATAGATAGGACCAAGTGTAGATCAAAACCTGATACAGTTT 606
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LOCUS Sequence 8 from Patent WO03004523.
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ACCESSION AX671108  
VERSION AX671108.1 GI:29329570  
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